US-08-455-683-12.rspt

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Feb 17 11:16:36 2000; MasPar time 22.82 Seconds 705.631 Million cell updates/sec not generated. Tabular output Run on:

>US-08-455-683-12 (1-295) from US08455683.pep 2229 1 YTKWKTATNIYIFNDALADA......NTVQDPAYLREIDGMMNKPV 295 Title: Description: Perfect Score: Sequence:

179066 seqs, 54579741 residues PAM 150 Gap 11 Searched:

Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptremb19 1.sp\_archea 2.sp\_bacteria 3.sp\_fungi 4.sp\_human 5.sp\_invertebrate 6.sp\_mammal 7.sp\_mhc 8.sp\_organelle 9.sp\_phage 10.sp\_plant 11.sp\_rodent 12.sp\_unclassified 13.sp\_vertebrate 14.sp\_virus

Mean 47.211; Variance 119.565; scale 0.395 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Pred. No.	5.90e-223	1.22e-212	5.58e-113	1.23e-78	6.54e-58	4.56e-58	1.34e - 57	.13e-5	2.32e-51	6.78e-51	.74e-5	5.78e-50	.04e-	5.78e-50	5.78e-50	2.41e-49	3,446-49	2.91e-48	4.15e-48	5.93e-48
Description	IOICI	MU-OPIOID RECEPTOR.	OPICID RECEPTOR, KAPPA	DELTA OPIOID RECEPTOR/	EG:121E7.2 PROTEIN.	GALANIN RECEPTOR GALR2	GALANIN RECEPTOR TYPE	CHEMOKINE RECEPTOR CCR	CXCR4.	G-PROTEIN COUPLED RECE	G PROTEIN COUPLED P2Y	CCR5 RECEPTOR (FRAGMEN	CCR5 RECEPTOR (FRAGMEN	CCR5 RECEPTOR (FRAGMEN	GALANIN 2 RECEPTOR HOM	CCR5 RECEPTOR (FRAGMEN	CARDIOEXCITATORY RECEP	G PROTEIN-COUPLED RECE	CCR5 RECEPTOR (FRAGMEN	RECEPTOR PROTEIN CKR3.
A	575	042324	060733	064206	076873	043603	088854	077776	093247	035811	057466	014694	018770	015538	060755	018772	044426	609680	018771	055169
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% Query Match Length	373	383	117	119	263	387	371	352	353	361	374	333	352	352	368	352	465	383	352	359
% Query Match	68.3	65.5	38.4	28.8	23.0	23.0	22.9	21.2	21.1	21.0	21.0	20.7	20.7	20.7	20.7	20.5	20.5	20.2	20.1	20.1
Score	1523	1461	856	643	512	513	510	472		467										
Result No.		2	m	4	IJ	9	7	ω	on	10	11	12	13	14	15	16	17	18	13	20

258 RNMRRITRMVLVVVAAFIICWIPIHIFIIEKTLVDINQKNPFVIASWHLHRT-GYTNSSL 316 

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                                                                                                                                                                                                                CATOSTOMUS COMMERSONI (WHITE SUCKER).
BUKARYOTA, WETAZOA, CHORDARA; VERTEBRAYA, TELEBOSTEI; NEOPIERYGII;
TELEBOSTEI; EUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; COBITOIDEA;
CATOSTOMIDAE; CATOSTOMUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 PLQVSNFDCTLLFPHPPW-YWETLLKICVFILAFIMPVLIITVCYGLMILRLKSVRMLSG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 YTKMKTATNIYIFNLALADALATSTLPFQSVNYLMGTWPFGDVVCKIVMSIDYYNMFTSI 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 FILITMSIDRYIAVCHPVKALDFRIPRNAKIVNVCNWILSSAIGLPVWVMASTITIBNQNS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 SKEKDRNLRRITRMVLVVVAVFIICWTPIHIFVIIKALVTIPNSLFQTVTWHFCIALGYT 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YTKMKTATNIYIFNLALADALVTTTMPFQSTVYLMNSWPFGDVLCKIVISIDIYNMFTSI 60
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE-CR.NS;
TISSUE-CR.NS;
TARADA M.G., HARVEY R.J., GRETEN F.R., KREIENKAMP H.J., ZWIERS H.,
STHMER T., LEDERIS K., RICHTER D.,
STHMER T., LEDERIS K., BICHTER D.,
STHMER T., LEDERIS K., RICHTER D.,
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
EMBL; Y10904; E1169530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBMITTED (NOV-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
EMBL; U16998; G595937; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUIHERIA;
SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
0PIOID RECEPTOR, KAPPA 1 (KAPPA OPICID RECEPTOR) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
PFAM; PF00001; 7tm_1; 1.
G-PROTEIN COUPLED RECEPTOR; IRANSMEMBRANE; GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00001; 7tm 1; 1.
G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
                                                                                                                        LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 NSSINPILYAFIDENFKRCFRDFCFPLKMXMERXSISRVRN 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1461; DB 13;
Pred. No. 1.22e-212;
50; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     00BBDCBD CRC32;
                                 383 AA.
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PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
                                                                                             CREATED)
                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43232 MW;
                                                                                       01-JAN-1998 (TREMBLREL. 05, 01-JAN-1998 (TREMBLREL. 05, 01-NOV-1998 (TREMBLREL. 08, MG-OPIOID RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.5%;
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Conservative
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                              PRELIMINARY;
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ses 183; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     383 AA;
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LT 2
042324
042324;
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DELTA OPIOLD RECEPTOR/DOR (FRAGMENT).
MUCS MUSCELUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 96211868.

ROY S., SEDQI M., RAMAKRISHNAN S., BARKE R.A., LOH H.H.;

ROY S., SEDQI M., RAMAKRISHNAN S., BARKE R.A., LOH H.H.;

"Differential effects of opioids on the proliferation of a macrophage cell line, Bac 1.2F5.";

CELL. IMMUNOL. 169:271-277(1996).

EMBL; S81965; E257299; -.

PRAM; PF00001; 7tm_1; 1.

NOW_TER
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                                                                                                                                                                                                                                                                                                                                                                                      1 YIKWKTAINIXIENLALADALVITIMPEQSIVYLMNSWPFGDVLCKIVISIDYNNETSI 60
                                                                                                                                                                                                                                                                                                                         1 YTKMKTATNIYIFNLTLADALVTTTMPFQSAVYLMNSWPFGDVLCKIVISIGYYNMFTSI 60
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                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 FILTHMASVDRYIAVCHPVKALDFRTPLKAKIINICIWLLASSVGISAIVLGGTKVRE 117
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MORPHY L., HARRIS D., BARRELL B.;
"Sequencing the distal X chromosome of Drosophila melanogaster.";
SUBMITTED (JUN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
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01-NOV-1998 (TREMBLEEL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLEEL. 08, LAST SEQUENCE UPDATE)
EG:121E7.2 PROPEIN.
EG:121E7.2.
DROSOPHILA MELANOGASTER (FRUIT FLY).
BROSOPHILA MELANOGASTER (FRUIT FLX).
PURARYOTA; METAZOA; ARTHROPODA; TRACHERATA; HEXAPODA; INSECTA;
PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
                                                                                                                              Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 119;
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                                                                                                                         Score 856; DB 11; 1
Pred. No. 5.58e-113;
3; Mismatches 1;
117
13070 MW; FCCF68E1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                   Query Match 38.4%;
Best Local Similarity 96.6%;
Matches 113; Conservative
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Matches 81; Conservative
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117 1
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MEDLINE; 96211868.
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SEQUENCE
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076873;
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6 TATNIYIFNLALADA-LVTTTMPFQSTVYLMNSWPFGDVLCKIVISIDYYNMFTSIFTLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 ILYAFLDENFKRCFRDFCFPLKMXMERXSTSRV 274
                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                       01-NOV-1998 (TERMBLEEL. 01-NOV-1998 (TERMBLEEL. GALANIN RECEPTOR TYPE 2.
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tes 82; Conser
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SEQUENCE FROM N.A.
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01-NOV-1998
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077776;
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Matches
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AC 07
DT 01
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                                                                                                                                                                                                                                            LIMMSVDRYIAVCHPVKALDFRIPLKAKIINICIWLLSSSVGISAIVLGGIKVREDVDVI 122
                                                                                                                                                                                                                             --Y-AFSA--FC--ILF-QVSFFLSSYVAP-LTLI-CFLYMGMLARLWKSAPGCKPSAES 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STINLFILNLGVADLCFILCCVPFQATIYTLDGWVFGSLLCKAVHFLIFLIMHASSFTLA 117
                                                                                                                                                                           61 LVLMSFDRFLAVVHPVTSMSLRIE-RNATLYLSPWLLTNSSDKNQSVPDLAQTQQKI-FI 118
                                                                                                                          1 MRSITNLLIINLAVSDILFVIFCVPFTATDYVLPEWPFGNVWCKFVQYMIVVTCHCSVYT 60
                                                                                                   Gaps
                                                                                                                                                   4 MKTAINIYIENLALADAL-VITIMPFQSTVYLMNSWPFGDVLCKIVISIDYYNMFTSIFT
                                                                                                                                                                                                                                                                              RKGKRRVTRMVVVVVLAFAICWLPIHVILVLKALNLYGGSHLSVIIQIISHVVAYTNSCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FATHI Z., BATTAGLINO P.M., IBEN L.G., LI H., BAKER E., ZHANG D., MCGOVERN R., MAHLE C.D., SUTHERLAND G.R., IISNAA T.P., DICKINSON K.E.J., ANTAL ZIMANYI I., SUBMIITED (APR-1999) TO EMBLYGENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (3)
SEQUENCE FROM N.A.
KULAKOWSKI L.F. JR., BROUSSARD S.R.;
KOLAKOWSKI L.F. JR., BROUSSARD S.R.;
"Galanin Receptor Type 2 (GalR2) from Human and Mouse: Genomic Cloning, Chromosomal Localization, Functional Expression, Gq Dependent Signal Transduction, and Expression Pattern.";
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDSJ DATA BANKS.
EMBL; AF046050, G2921760; --
EMBL; AF042782; G3642914; --
EMBL; AF042782; G3642914; --
TOTHER 387 AA: 41700 MW; E7A343C3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE, 98153789.
MEDLINE, BESTROWN S. ZHELNIN L., BROWN S.-E.,
GORE-WILLSE A.R., GREGOR P., CORNFIELD L.J.;
"Cloning and expression of the human galanin receptor GalR2.";
BIOCHEM. BIOPHYS. RES. COMMUN. 243:474-479(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 513; DB 4; Length 387;
Pred. No. 4.56e-58;
85; Mismatches 87; Indels 14;
                                                                                                   16;
                                                                        Length 263;
                          EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                        ; DB 5; I
6.54e-58;
                       SUBMITTED (JUN-1998) TO EMBL/GENBANK/DDBJ DATA
EMBL; AL024454; E1301584; -.
SEQUENCE 263 Aa; 29891 MM; D89F6C55 CRC32;
                                                                                     Pred. No. 6.54e-
                                                                                                                                                                                                                                                                                                                                                                                                          387 AA.
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CATARRHINI; HOMINIDAE; HOMO
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Best Local Similarity 32.1%;
Matches 88; Conservative
                                                                                        35.4%;
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                                                                                                                                                                                                                                                                                                                                               Local Similarity 35.4%;
nes 91; Conservative
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01-JUN-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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HOMO SAPIENS (HUMAN)
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SEQUENCE FROM N.A.
             BENOS P.;
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043603;
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Matches
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BUKARYOTA, BUTAZOA, TORORATA, VERTEBRATA; MAMMALIA, EUTHERIA, RODENIIA,
SCIUROGRAFII, MURLDAE, MURINAE, MUS.
                                                                                                                                                                                                                                                                                                              288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 AVSLDRYLAIRYPMHSRELRIPRNALAAIGL-IWGLAL-L-FSGPYLSYYS-QSQLANLI 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54
64
                                                                                                         65 MMSVDRYIAVCHPVKALDFRTPLKA-KIINICIMLLSSSVGISAIVLGGTKVREDVDVIE
                                                                                                                                                                                                                                                                                                                                                      118 AVSLDRYLAIRYPLHSRELRIPRNALAAIGL-IWGLSL-L-FSGPYLSYYR-QSQLANII
                                                                                                                                                                                   VC-H-PAWSAPRRRA-MDICTFVFSYLLPVLVLGLTYA-RTLRYLWRAVDPVAAGSGARR
                                                                                                                                                                                                                                             124 CCLQPPDDDYSWWDLFMKICVFIFAFVIFVLIIIVCYTLMILR-L-KXV-RLLSGSREKD
                                                                                                                                                                                                                                                                                                              230 AK-RKVTRMILIVAALFCLCWMPHHALILCVWFGQFPLTRATYALRILSHLVSYANSCVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 CCLQFPDDDYSWWDLFMKICVFIFAFVIPVLIIIVCYTLMILR-L-KXVRLLSGSREKDX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91; Indels 12;
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Pred. No. 1.34e-57;
88; Mismatches 91; Indels 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COLAKOWSKI L.F. JR., BROUSSARD S.R.;
"Galanin Receptor Type 2 (Galk2) from Human and Mouse: Gen
"Galanin Receptor Type 2 (Galk2) from Human and Mouse: Gen
Cloning, Chromosomal Localization, Fructional Expression,
Dependent Signal Transduction, and Expression Pattern.";
SUBMITTED (JAN-1998) TO MBEL/GENBANK/DDBJ DATA BANKS.
EMBL: AF042784; G3642918; ".
SEQUENCE 371 AA; 40533 WW; FF7FBAOC CRC32;
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RATTUS NORVEGICUS (RAT).
EUKARYOTA, METAZOA, CHORDATA, VERTEBRATA, MAMMALIA, EUTHERIA, RODENTIA,
SCIUROGNATHI, MURIDAE, MURINAE, RATTUS.
                                                                                                                                                                  TLTMMSVDRYIAVCHPVKALDFRTPLKAKIINICIWLLSSSVGISAIVLGGTKVRE-DVD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 DITLPEE-FDHYVYFSSA-VMVLLFGLPFLLITLVCYGLMARRL-Y-RPLPGAGQSSSRLR 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 RITRLVLVVVAVFVVCWTPIHIF -- ILVEA--LGSTSHSTAALSSYY-FCIALGYTNSSL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 ATATYMFHLALSDTLYVLSLPTLVYYYAARNHWPFGTGLCKFVRFLFYWNLYCSVLFLTC 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 ATNIYIFNLALADALVTTTMPFQSTVYL-MNSWPFGDVLCKIVISIDYYNMFTSIFTLTM 65
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                                            182 TI-CELTYPLQGNTVWKAVFRFQHIFV-GFLLPGLIILTCYCIIISKL-S-K--N-SKGQ
                                                                                                                                      235 ALK-RKALKTTVILILCFFICWLPYCAGILVDTLVMLNVISHTCFLEQGLEKWIFFTEAL
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LAST SEQUENCE UPDATE)
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Pred. No. 6.78e-51;
67; Mismatches 97;
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                                                                                                                                                                                                                                294 AYFHCCLNPILYAFLGVKFSKSARN 318
                                                                                                                                                                                                                                                                          257
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                                                                                                                                                                                                                                                              233 GYTNSSLNPILYAFLDENFKRCFRD
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ilarity 31.5%;
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(TREMBLREL.
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nes 82; Conserv
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035811;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 움
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps 17;
                                       EUKARYOTA, METAZOA, CHORDATA, VERTEBRATA, MAMMALIA, EUTHERIA, PRIMATES,
CATARRHINI, CERCOPITHECIDAE, CERCOPITHECINAE, CERCOCEBUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYPRINUS CARPIO (COMMON CARP).
EUKARYOIA: METRAGA; CHORDAIA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI: EUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; CYPRINOIDEA;
CYPRINIDAB; CYPRININAE; CYPRINGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                  RIKSMIDIYLLINLAISDILFILIVPF-WAHYAAAQWDFGNIMCQLLIGLYFIGFFSGIFF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSKNMTDKYRLHLSIADLLFVLTLPF-WAVDAASGWHFGGFLC-VTVNMIYTLNLYSSVL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IIILTIDRYLAIVHAVFALKARTVIFGVVISVITWVVAVFASLÞGIIFTRSQ-REGLHYT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 ILAFISLDRYLAVVRATNSQNFRRVLAEKVIYLGVWLPASLLITVPDLVF--AKVHDIGMN 181
                                                                                                                                                        CHEN Z., KWON D., JIN Z., MONARD S., TELFER P., JONES M., LU C.,
AGUILLAR R., HO D.D., MARX P.A.;
"Natural infection of a homozygous delta 24 CCR5 red-capped mangabey
with a R2b-tropic simian immunodeficiency virus.";
J. EXP. MED. 0.0-0.(1938).
BENBL, AF084004; G3694849.
SEQUENCE 352 AA. 40475 MW; 6649F573 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUJIKI K., NAKANA.

FUJIKI K., NAKANA.

"CDNA cloning of a carp homologue of mammalian CXCR4.";

"CDNA cloning of a carp homologue of mammalian CXCR4.";

"CDNA cloning of a carp homologue of mammalian CXCR4.";

"SABMITTED (MAR-1998) TO EMBLACABNBANK/DDBJ DATA BANKS.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROPEIN COUPLED RECEPTORS.

-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

PROSITE; PSO(0237, G_PROTEIN RECEPTOR; 1.

G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.

SEQUENCE 353 AA; 39633 MW; 23DD5347 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 -CSPHFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYS-GIL--KT--LLR-CRN-EKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 ECCLQFPDDDYSWWDLFMKICVFIFAFVIPVIIIVCYTLMILRIKXVRLLSGSREKDXN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RHRAVRLIFTIMIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85; Indels 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 470; DB 13; Length 353;
Pred. No. 2.32e-51;
76; Mismatches 85; Indels 22
                                                                                                                                                                                                                                                                                                                                           Score 472; DB 6; Length 352;
Pred. No. 1.13e-51;
83; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ... .. . . . . . . . . . . . . . . .
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08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 SSLNPILYAFLDENFKRCFRDF 258
                   CERCOCEBUS TORQUATUS TORQUATUS.
                                                                                                                                                                                                                                                                                                                                           21.2%; ilarity 28.6%; conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 30.9%;
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
es 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                      STRAIN=1208
                                                                                                                                                                                                                                                                                                                                              Query Match
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093247
093247;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     09
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184 297

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CHORDAIA; VERTEBRAIA; MAMMALIA; EUTHERIA; PRIMATES;
                                                                                                                                                                                                                                                                                                                                EUKARYOTA; METAZÒA; CHORDATÁ; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; PAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 RLKSMTDIYLLNLAISDLLFLLTVPF-WAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFF 118
                                            123 ECCLQFPDDDYSWWDLFMKICVFIFAFVIPVLIIIVCYTLMILRLKXVRLLSGSREKDXN 182
                                                                                  211 RHRAVRLIFTIMIVYFLFWAPYNIVLLINTFQEFFGLNNCSSSNRLDQAMQVTETLGMTH 270
                                                                                                 183 LRRITELVLYVVAVEVVCWTPIHI-FIL-V-EAL-G-STSHSTAALS-SYYFCIALGYTN 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -CSSHFPYSQYQFWKNFQTLKMVILGLVLPLLVMVICYS-GIL--KT--LLR-CRN-EKK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230 RHRAVRLIFTIMIVYFLFWAPYNIVLLINTFQBFFGLNNCSSCNRLDQAMQVTETLGMTH 289
 63 LIMMSVDRYIAVCHPVKALDFRIPLKAKIINICIWLLSSSVGISAIVLGGTKVREDVDVI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 IILLIIDRYLALVHAVFALKARTVIFGVVTSVITWVVAVFASLPGIIFTRSQ-REGLHYT 177
                                                                                                                                                                                                                                                                                                                                                                                                      ZHANG L., CARRUTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 KMKTAINIYIPNLALADALVITIMPFQSIVYLMNSWPFGDVLCKIVISIDYYNMFTSIFT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159 -CSSHFPYSQYQFWKNFQTLKIVILGLVLPLLVMVICYS-GIL--KT--LLR-CRN-EKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 462; DB 6; Length 352;
Pred. No. 4.04e-50;
82; Mismatches 89; Indels 16;
                                                                                                                                                                                                                                                              LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                        352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               352
                                                                                                                                                                                                                                                                                                                                                                                                                  HO D.D.;
AIDS RES. HUM. RETROVIRUSES 0:0-0(1997)
                                                                                                                                                                                                                                                   CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                        PRT;
                                                                                                                                        292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 SSLNPILYAFLDENFKRCFRDF 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             290 CCINPIIYAFVGEKFRNYLLVF 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352 352
352 AA; 40523 MW;
                                                                                                                                                                                                                                                                                                                       PAN TROGLODYTES (CHIMPANZEE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05,
                                                                                                                                                                                                                                                01-JAN-1998 (TREMBLREL. 05, 01-JAN-1998 (TREMBLREL. 05, 01-NOV-1998 (TREMBLREL. 08, CCR5 RECEPTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTA; METAZOA; CHORDAT;
CATARRHINI; HOMINIDAE; HOMO
                                                                                                                                        271 CCINPIIYAFVGEKFRNYLLVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF011538; G2305194;
PFAM; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 28.6%;
nes 75; Conservative
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01-JAN-1998 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
CCR5 RECEPTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
STRAIN=MACCR5-140A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
SEQUENCE
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015538
015538;
                                                                                                                                                                                                        7LT 13
018770
018770;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
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Matches
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                                                                                                                                                                                                                                                                 12;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                          75 ATTIYMFNLAISDILYVFSLPTLVYYYADRNNWPFGKVFCKIVRFLFYANLYSSILFLTC 134
                                                                                                                                                                                                                                                                                                                                                135 ISVHRYMGICHPIRSLKWVKTKHARLICVGVWLVVTICLIPNLIFVTISSKDN-STL-CH 192
                                                                                                                                                                                                                                                                                                                                                                           125
                                                                                                                                                                                                                                                                                                                                                                                                      DTTKPEEFDHYVHYSS-SIMALLFGIPFLVIVVCYCLMAKRL-CKRSFPSPSPRVPSYKK 250
                                                                                                                                                                                                                                                                                                                                                                                                                               184
                                                                                                                                                                                                                                                                                                                                                                                                                                                            310
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Ω
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                       protein-coupled P2Y
                                                                                                                                                                                                                                                                                                                                                                :|| ||:::|||:::|
66 MSVDRYIAVCHPVKALDFRTPLKAKIINICIWLLSSSVGISAIVLGGTKVREDVDVIECC
                                                                                                                                                                                                                                                                                                                                                                                                                      G., HAHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 RLKSMTDIYLLNLAISDLFFLLIVPF-WARYAAAQWDFGNTMCQLLTGLYFIGFFSGIFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RSIKMIIIVLTVFAICFVPFHITRTLYYTSRYFQADCQTLNIINFTYKITRPLASINSCL
                                                                                                                                                                                                                                                                 13;
                                                        EUKARYOTA; METAZOA, CHORDATA; VERTEBRATA; ARCHOSAURIA, AVES;
NEOGNATHAE; GALLIFORMES; MELEAGRIDIDAE; MELEAGRIS.
                                                                                                                                                                                                                                      Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 461, DB 4; Length 333;
Pred. No. 5.78e-50;
84; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. ZHANG I., CAN Y., WANG ZHANG I., CAN Y., WANG
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
-NOV-1998 (TREMBLREL, 08, LAST ANNOTATION UPDATE) PROTEIN COUPLED P2Y NUCLECTIDE RECEPTOR.
                                                                                                                                                                                                                                    Score 468; DB 13; I
Pred. No. 4.74e-51;
75; Mismatches 92;
                                                                                                                                                       an avian G
                                                                                                                                                                 receptor.";
MOL. PHARMACOL. 52:928-934(1997).
EMBL; AF031897; G2707256; -.
SHOIFNCE 374 AA; 42594 MW; 5320428C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 AA; 38174 MW; DC2CD1E3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HO D.D.;
AIDS RES. HUM. RETROVIRUSES 0:0-0(1997)
                                                                                                                                                                                                                                    21.0%; Score 468;
larity 29.1%; Pred. No. 4
Conservative 75; Mismat
                                                                                                             IISSUE=BLOOD;
MEDLINE; 98086419.
BOYER J.L., WALDO G.L., HARDEN T.K.;
"Molecular cloning and expression of
                                           MELEAGRIS GALLOPAVO (COMMON IURKEY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 12 014694 014694;
014694;
01-7aN-1998 (TREMBLREL: 05, CI
01-7aN-1998 (TREMBLREL: 08, LL
01-NOV-1998 (TREMBLREL: 08, LL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.7%; s.larity 28.2%; F. Conservative 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF011504; G2305126;
PFAM; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCR5 RECEPTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|||| |: ::::
NPILYAFLD-ENFK 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 DPILY-FWAGDKYR 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                  Best_Local Similarity
Matches 74; Conser
                                                                                                  SEQUENCE FROM N.A.
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01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLERL. 08, LAST ANNOTATION UPDATE)
GALANIN 2 RECEPTOR HOMOLOG.
HOMO SAPIENS (HUMAN).
BUKARYOTA; METAZOA; CHORDATA; VERIEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
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ZHANG L., CARRUTHERS C.D., HE I., HUANG Y., CAO Y., WANG G., HAHN
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SECULE FROM N.A.
MEDLINE; 98389766.
SMITH K.E., WALKER M.W., ARIYMYSHYN R., BARD J., BOROWSKY B.,
TAMM J.A., YAO W.-J., VAYSSE P.J.-J., BRANCHEK T.A., GERALD C.,
JONES K.A.,
Cloned human and rat galanin GALR3 receptors. Pharmacology and
activation of g-protein inwardly rectifying k+ channels.",
J. BIOL. CHEM. 273:23321-23326(1998).
EMBL, AF067733; G3176927;
EMBL, AF0677399; G3608410,
SEQUENCE 368 AA, 39573 MW, 2DF74618 CRC32;
                                                                                                                                                                                                           Score 461; DB 4; Length 352;
Pred. No. 5.78e-50;
84; Mismatches 88; Indels 16;
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BENETT M.M., LESCOS M.K., GALLIPOLI P.Z., RAMABHADRAN T.V.;
SUBMITITE (MAY-1998) TO EMBL/GENBANK/DDBJ DAIA BANKS.
                                                                                                                                                                         40552 MW; B1ECA8D9 CRC32;
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EMBL; AF011516; G2305150; -.
EMBL; AF011534; G2305186; -.
EMBL; AF010501; 7tm_1; 1.
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SEQUENCE 352 AA; 40552 MW;
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Db 115 AVSVDRYLAVRHPLRSRALRTEFXARARYGL-VWILAALFSAPYLSYYGT-VR--YGALE 170

QY 65 MMSVDRYLAVCHPVRALDFRPLKAKI-INICIMLLSSCHISLIVLGGTKVRFDUDVE 123

Db 171 LCVPAWEDA-RRRAL--DVATEAAGYLLEVAVGSRTLRFLWAAVGPAGAAAEARR 227

QY 124 CCLCPFDDDYSWMDA-RRICVFIRAEVIPVLILIVCY--TLMILRIKXVRLLSGSRE-KD 180

Db 228 RATGRAGARALAALWGFHAEVIPVLILICFWYGREASPATACRLASHCLAYANSCLN 287

QY 181 XNLRITRLVLVVVAVFVVCWTPIHIFILCFWYGREASSYFFCIALGYTNSSLN 240

Db 288 PLVYALASRHFRAEFRRAPFRHRARRARRALRRVRPASSGPP 331

QY 121 PILYARLDENFKRCFRDF--CFPLKMXMERXSISRYRNIVQDPA 282
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Search completed: Thu Feb 17 11:17:01 2000 Job time: 25 secs.

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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using sw model OM nucleic - nucleic search, Run on:

February 17, 2000, 09:39:05; Search time 66.73 Seconds (without alignments) 5286.540 Million cell updates/sec

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Transgenic animals defective in one type of opioid receptor - used transgenic animals defective in one type of opioid receptor - used to identify agents for treatment of pain, drug addiction and transplant rejection, lacking side effects of known opiate(s) by transplant rejection, lacking side effects of known opiate(s) by isolosure; Fig 13; SBp; French.

Compission of the sequence is used to generate a transgenic receptor protein. The sequence is used to generate a transgenic computated with opiate receptors. In the mammal, the expression of associated with opiate receptor is modified, particularly by the gene encoding the opiate receptor is modified, particularly by the deletion of an exon and/or insertion of an arker gene, e.g. the nempton of saltered in nervous tissue. The agents are potentially of the gene is altered in nervous tissue. The agents are potentially of the gene is altered in nervous tissue. The agents are potentially consecuted or treatment of transplant rejection (as immunosuppressants). The method may isolate and identify powerful analgesics that lack morphine-like side effects.
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                                                                                                                                                                                                                                                                                                                                                                                                                Mouse kappa opiate receptor gene.

Mouse: kappa opiate receptor; transgenic animal; mammal; identification;
exon; nervous tissue; pain; drug addiction; transplant rejection;
immunosuppressant; analgesic; morphine; side effect; ds.
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11-JUL-1996; FR-008810.
(CNRS.) CENT NAT RECH SCI.
Dierlich A, Kieffer BL, LeMeur M, Matthes HWD, Simonin WPI; 98-10582/10.
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100.0%; Pre
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/product= ")
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                                                                           AACTIGGCTTIGGCAGAIGCTIIGGTTACTACGACTAIGCCCTTICAGAGIGCTGTCTAC
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01-DEC-1995 (first entry)
01-DEC-1995 (first entry)
Mammalian Kappa opioid receptor; mouse delta opioid receptor; analgesic; amplification; primer; rat; probe; E.coli; RT-PCR; hypnotic compound; ds.
                                                                                                                                                                                                                                                                                                                                                                            properties
Claim 2; Page 9-10; 15pp; Japanese.
The nucleotide sequence of the novel mammalian kappa opicid receptor
The nucleotide sequence of the novel mammalian kappa opicid receptor
DNA. The gene was isolated by amplifying a fragment from rat brain mRNA
by reverse transcriptase-PCR (RT-PCR) using primers Q8672-7 derived from
Plasmid pCRII to produce pRII. The plasmid pRII was used to probe a rat
Drain DNA library in lambda ZaPII to obtain a clone of the rat kappa
D.coli JM109 for production of the receptor protein. The receptor protein
Is useful for screening of analgesic and hypnotic compounds including
Sequence 2481 BP; 529 A; 588 C; 544 G; 770 m.
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635
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Pred. No. 1.1e-52;
0; Mismatches 3; Indels (
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                                                                                                                                                                                                                                                                                                                                                     Kappa opioid receptor protein and cells expressing it - us for the screening of compounds for analgesic and hypnotic
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                                                   1381 CTTGGTTTAACCCAGATTACAACTGCAG
                                      CTIGGTITAACCCAGAITACAACTGCAG
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30-JUL-1993, 190261.
09-JUL-1993, DP-170591.
(TAKE) TAKEDA CHEM IND LTD.
WPI: 95-144857/19.
                                                                                                                         Q86725 standard; cDNA; 2481
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98.98;
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Best Local Similarity
Matches 275; Conserv
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Key
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Pressing modified G protein property with a selective activation of target cell expressing modified G protein coupled receptor - allows control of cellular proliferation, coupled receptor - allows control of cellular proliferation, coupled receptor - allows control of cellular proliferation, coupled receptor that is activated superiorly by synthetic ligands. This cDNA sequence encodes Rasked superiorly by synthetic ligands. CC coupled receptor that is activated superiorly by synthetic ligands. CC coupled receptor that is activated superiorly by synthetic ligands. CC coupled receptor that is activated superiorly by synthetic ligands. CC coupled receptor that a coupled receptor for selective and contain a mind of the delta opioid receptor. The ORI comprises in the contain and epitope peptides to facilitate the detection and purification of recombinant ORIN. A novel method for selectively purification of recombinant ORIN. A novel method for selectively curification of recombinant oRIN. A novel method for selectively purification of recombinant oRIN. A novel method for selectively contrained acid sequence (1) that expresses a RASKL (A) and ccill a nucleic acid sequence (1) that expresses a RASKL (A) and ccill arresponse associated with receptor activation coupled (B) that bind to and activate (A), inducing the operation coupled (CC callular response associated with receptor activation of activate (CC callular implants comprising a TC transfected with (1): a cultivated (1): and transgenic cells including heterologus (1) in the Also new are: transgenic cells including heterologus (1) in the contraction of a cellular implants comprising a TC transfected (1): activated (1): activated (1): activated (1): and transgenic cells including the relatively few secretion of a cellular implants comprise comprise control of a cellular implants of the expenses of the respense of the response that can be required cell that are successfully transferded during gene therapy contraction, or stimularly in designed to expand the relative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cardiac arrhythmia, symptoms of bone disease, seizures, vascular contractions, dementia, neurodegeneration etc., for use as models of these diseases (claimed). The transgenic animals are also used for production of improved food products (e.g. increased calcium content in eggshells or altered fat/lean ratios) or to control
                      Human kappa opioid receptor prototype RASSL ORL DNA. Selective target cell activation; G protein-coupled receptor; RASSL; gene therapy, cell proliferation; kappa opioid receptor; human; transgenic animal; arrhythmia; bone disease; seizure;
                                                                                                                                                                                                                                                                                                                                                                 /note= "delta opioid receptor sequence"
                                                                                                                                                                                                                                                                                              /product= FLAG-modified KOR-HA fusion
                                                                                                                                                                                                                                     prolactin signal sequence
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                                                                                                              vascular contraction; disease model; ss.
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1275 BP; 266
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91. .1284
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                                                                                                                                             Chimeric - Homo sapiens.
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                                                                                                                                                                 Chimeric - Synthetic.
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26-MAR-1996; US-6223
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P-PSDB; W30299.
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                                                                                                                                                                                           Key
sig_peptide
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Query Match 5.5%; Score 77; DB 1; Length 1275; Best Local Similarity 100.0%; Pred. No. 8.1e-29; Indels Matches 77; Conservative 0; Mismatches 0; Indels
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Polymericetides and peptides derived from opioid receptor
Polymericetides and peptides derived from opioid receptor
Polymericetides - for useful drug substances.

Tolaim 10; Page 236-239; 300pp; English.

Elsim 10; Page 236-239; 300pp; English.

Ca partial nucleotide sequence of the novel human kappa opioid receptor

Ca partial nucleotide sequence of the novel human brain hippocampus CORA Library

Ca partial nucleotide sequence of the novel main hippocampus CORA Library

Ca sing a probe from the mouse kappa opioid receptor gene (Q75956). The

cusing a probe from the mouse kappa opioid receptor sequence of the

covery similar to the mouse kappa opioid receptor sequence. Of the

covery similar to the mouse vappa opioid receptor sequence.

C terminal 293 amino acids, 281 residues are identical and 6 residues

C terminal 293 amino acids, 281 residues are identical and conservative substitutions. The gene encoding the human opioid

c receptor can be placed in a suitable expression vector for production of

the protein in a cell. The opioid receptors thus produced are useful for

the protein in a cell. The opioid receptors proteins, for use in

capable of interacting with the opioid receptor proteins, for use in

capable of interacting with the opioid receptor proteins, for use in

capable of sequence 1000 BP; 238 A; 255 G; 278 T;
                                                                                                                                                                                                                                                 Human kappa opioid receptor partial cDNA fragment.

Mouse, kappa, delta; mu; opioid receptor; brain; primer; PCR; amplify; transsmenbrane domain; somatostatin; receptor; human; expression vector; truncate; chimaeric; assay; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Human kappa opioid receptor oDNA.
Human; kappa opioid receptor; psychiatric disorder; cardiovascular; neurology; diagnosis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/product= partial human kappa opioid receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= kappa_opioid_receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.3%; Score 32; DB 1;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 32; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            474 TACATATTTAACCIGGCTTIGGCAGAIGCTIT 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 TACATATTTAACCTGGCTTTGGCAGATGCTTT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I12550 standard; cDNA; 1142 BP. I12550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reisine T, Yasuda K;
                                                                                                                                                                                                      .1142
                                                                                                              562 AIGAIGAGIGIGGACCG 578
                                                                                                                                                                                                                                                                                                                                                                                   102. .989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-DEC-1994.
20-MAY-1994; U05747.
20-MAY-1993; US-066296.
30-JUL-1993; US-100694.
05-NOV-1993; US-147592.
(ARCH-) ARCH DEV CORP.
Bell GI, Relatine T, Ya.
WPI; 95-022804/03.
                                                                          636 ATGATGAGTGTGGACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                   Q75931;
18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9428132-A.
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075931
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P-PSDB; W30298
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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This CDNA sequence comprises the coding region for human kappa opioid receptor (KOR, see W30297), a G protein-coupled receptor implicated in neurotransmission. A novel method for selectively activating a target cell (TV) comprises: (i) introducing into the activating a target cell (TV) comprises: (i) introducing into the activating a target cell (TV) comprises: (i) introducing into the activating a mucleic acid sequence (I) that expresses a G protein-coupled receptor (A) modified to be activated superiorly by a synthetic receptor (II) exposing the transfected (A), inducing the receptor activation (A) has: (a) decreased binding affinity for a selected natural ligand of the native receptor; (b) binding affinity for activation. (A) has: (a) decreased binding affinity for a sclivated by binding (B) sufficiently to produce the required cellular response. Also new are: (1) transgenic cells including heterologous (I) in the genome; (2) cellular implants comprising a TC transfected with (I); (3) isolated (I); and (4) transgenic non-human animals expressing (A). Activation of (A)
                                                                                                                                                                                                                                                                              Claim 3; Page 13-15; 30pp; French.
This sequence codes for the human kappa opioid receptor and was obtained from two overlapping oDNs fragments isolated from a human placental cDNs library. The fragments were amplified from the library using PCR primers based on the sequence of human percent clones which hybridissed with a murine delta receptor cDNs probe. Nucleotide probes derived from the kappa opioid receptor cONs coding sequence are useful for diagnosis of neurological, cardio-vaccutar and psychiatric disorders associated with opioid
                                                                                                                                                                                                           New nucleic acid encoding the human Kappa opioid receptor - usef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-APR-1998 (first entry)

Human kappa opioid receptor cDNA,

Selective target cell activation; G protein-coupled receptor;

RASSL; gene therapy; cell prollferation; kappa opioid receptor;

human; transgenic animal; arrhythmia; bone disease; seizure;

vascular contraction; disease model; ss.
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/note= "incomplete termination codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       474 TACATATITAACCIGGCITIGGCAGAIGCTIT 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   289 TACATATTTAACCTGGCTTTGGCAGATGCTTT 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337 C;
                                                                  07-JUL-1995; F00912.
11-JUL-1994; FR-008531.
(UYST-) UNIV PASTBUR STRASBOURG LOUIS.
Kleffea Simonin F;
WPI; 96-097628/10.
P-PSDB; R88722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; W30297.
Selective activation of target cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T90998 standard; cDNA; 1143 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-001-1997,
25-MAR-1997, U05334,
26-MAR-1996, US-622348.
(REGC ) UNIV CALIFORNIA.
CONLLIN BR;
WPI; 97-502739/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1142 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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WO9735478-A1.
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                                                                                                                                                                                                                                                               modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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T90998
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Selective activation of target cell expressing modified G protein coupled receptor - allows control of cellular proliferation, especially for amplification of transfected cells in gene therapy. Example 1; page 77-79; 117pp; English.

This cDNA sequence encodes a polypeptide (see W30298) comprising the num of protein-coupled kappa optioid receptor (KOR) (see also W30299); lens a receptor Activated superiorly by a synthetic are receptor activated superiorly by a synthetic ligand. A novel method for selectively activating a target cell (TC) comprises: (i) introducing into the cell a nucleic acid sequence (I) that expresses a RASEL (A) and (ii) exposing the cransfected cell to small synthetic molecules (B) that bind to and activate (A), inducing the G protein coupled cellular response associated with receptor activation. (A) has: (a) decreased binding affinity for a selected natural ligand of the native receptor; (b) binding affinity to produce the required cellular response. Also new
results, in vitro or in vivo, in cellular proliferation, or secretion of a cellular product, particularly a heterologous therapeutic protein encoded by a second inserted nucleic acid sequence. Particularly it is used to expand the relatively few cells that are successfully transfected during gene tharapy procedures. Other responses that can be regulated are cell migration and contraction, or pigment production. In transgenic animals, expression or stimulation of (A) is designed to develop cardiac arrhythmia, symptoms of bone disease, seizures, vascular contractions, dementia, neurodegeneration etc., for use as models of these diseases (claimed). The transgenic animals are also used for production of improved food products (e.g. increased calcium content in eggshells or altered fat/lean ratios) or to control fertility or induce labour. A RASSL derived from KOR, designated C CDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-APR-1998 (first entry)
Human kappa opioid receptor modified cDNA.
Selective target cell activation, G protein-coupled receptor;
RASSL; gene therapy. cell proliferation, kappa opioid receptor;
human; transgenic animal; arrhythmia; bone disease; seizure;
vascular contraction; disease model; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.3%; Score 32; DB 1; Length 114
100.0%; Pred. No. 2e-06;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prolactin signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   289 TACATATITAACCIGGCITIGGCAGAIGCIIT 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         474 TACATATITAACCIGGCTTIGGCAGATGCTTT 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        337 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190999 standard; cDNA; 1284 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 A;
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/product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.35
Best Local Similarity 100.0
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91. .1284
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Chimeric - Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-1996; US-622348.
(REGC ) UNIV CALIFORNIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1143 BP;
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25-MAR-1997; U05334.
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08-MAR-1993 (first entry)
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                                                                                                                                                                                                                                                                                                                                           0;
are: transgenic cells including heterologous (I) in the genome; cellular implants comprising a TC transfected with (I); isolated (I); and transgenic animals expressing (A). Activation of (A) results, in vitro or in vivo, in cellular proliferation, or secretion of a cellular product, particularly a heterologous therapeutic protein encoded by a second inserted nucleic acid sequence. Particularly it is used to expand the relatively few cells that are successfully transfected during gene therapy procedures. Other responses that can be regulated are cell migration and contraction, or pigment production. In transgenic animals, expression or signal and designed to develop cardiac arrhythmia, symptoms of bone disease, seizures, vascular contractions, dementia, neurodegeneration etc., for use as models of these diseases (claimed). The transgenic animals are also used for production of improved food products (e.g. increased calcium fertility or altered fat/lean ratios) or to control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example: Fig 8b; 74p; Facilish.
To isolate opiate receptor genomic clones, 300,000 human genomic clones and a similar number of mouse genomic clones were probed with the 1.1 kb mouse delta opioid receptor clone DoR-1 Pst/Xbal fragment. One mouse clone and three human genomic clones were isolated. The 3 human clones had very different EcosI patterns which indicated that three different genes were represented by the human genomic clones which were designated H3, H14 and H20. H14 maps to chromosome 8. It encodes the human kappa opicid receptor.
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                                                                                                                                                                                                                                                                                                                                           Gaps
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DNA encoding opioid receptors and antibodies against this proceptor - used to express and locate these receptors, and screen cycs. for opioid (antyagonist activity
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Partial sequence of the human kappa opioid receptor genomic clone H14 (KORa).
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100.0%; Pred. No. 6.3e-06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                   322
                                                                                                                                                                                                                                                                                                              Score 32; DB 1;
Pred. No. 2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.AUG-1993; U07665.
13.AUG-1992; US-929200.
(REGC ) UNIV CALIFORNIA.
Edwards RH, Evans CJ, Kaufman D, Keith DE;
                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                           474 TACATATTTAACCTGGCTTTGGCAGATGCTTT 505
                                                                                                                                                                                                                                                                                                                                                                                                        400 IACATATTTAACCTGGCTTTGGCAGATGCTTT 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Opioid receptor; morphine; opiate; ss.
                                                                                                                                                                                                                                                                   377
                                                                                                                                                                                                                                                                                                  2.3%; Scc...
100.0%; Pre
                                                                                                                                                                                                                                                                     265 A;
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                                                                                                                                                                                                                                                       induce labour.
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Q29156;
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                                                                                                                                                                                                                                                                                                                  Query Match 2.3
Best Local Similarity 100.
Matches 32; Conservative
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Matches 31; Conserv
                                                                                                                                                                                                                                                                     1284 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                        fertility
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                                                                                                                                                                                                                                                                        Sequence
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Q56702
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Treating and detecting tumours e.g. pancreatic somatostatinoma treating and detecting tumours e.g. pancreatic somatostatinoma claim 18; Fig 10; 50pp; English.

A partial clone of purified pituitary somatostatin was used to design primers ICII and TM VII. Rat genomic DNA was subjected to PCR and rom the deduced location of the corresp. peptides i.e. TM VII and ICII, a 50l bp fragment of the receptor CDNA was obtd. This sequence was used in PCR to obtain the 5' rat brain SR sequence (some bases undefined and having a gap in the sequence). The receptor may be undefined and having a gap in the sequence). The receptor may be required to raise antibodies for detection and treatment of tumours in patients, and to treat e.g. pancreatic somatostatinoma, and to regulate the action of somatostatin in vivo.

See also 02914.7 and 035865-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-AUG-1995 (first entry)
Mouse opioid receptor-like receptor MOP2 cDNA.
Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
truncmenbrane domain; somatostatin; receptor; human; expression vector;
truncate; chimaeric; assay; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Brain somatostatin receptor 5' DNA.
SR; antibodies; tumours; glycoprotein; pancreatic somatostatinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= mouse opioid receptor-like receptor
                                                                                                                                                                                                                                                                                                                                                                                                    New somatostatin receptor, active fragments and antibodies prevents somatostatin binding to its receptor, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1%; Score 29; DB 1; Length 822; 100.0%; Pred. No. 6.2e-05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotides and peptides derived from opioid receptor polypeptides - for use in therapeutic compositions and in screening assays for useful drug substances. Claim 28; Page 225-229; 300pp; English.
                                                                                                                                                                                          14-0CT-1992.
25-MAR-1991.
28-MAR-1991.
28-MAR-1991.
28-MAR-1991.
28-MAR-1991.
(AMCY ) AMERICAN CYANAMID CO.
COT-LAN , Eppler CM, Hadcock J, Hulmes JD, Shieh H;
Strand J, Zyskjr, Cecil ME;
P-PSDB; R27505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              450 AAGATGAAGACCGCAACCAACATCTACAT 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
161. .1264
                                                                                             Location/Qualifiers
1. .822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reisine I, Yasuda K;
                                                                                                                                                 /*tag= a
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Best Local Similarity 100.
Matches 29; Conservative
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20-MAY-1994; UO5747.
20-MAY-1993; US-066296.
30-JUL-1993; US-10694.
05-NOY-1993; US-147592.
(ARCH-) ARCH DEV CORP.
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WPI; 95-022804/03.
P-PSDB; R67671.
                                                                            Rattus rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9428132-A.
                                                                                                                                                                         EP-508221-A
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Disclosure, Fig.1, 35pp. English.

Primers based on rodent opoid receptors were used to amplify rat genomic DNA. Products were re-amplified and subcloned into pCR-II vector and amplified in E. coli. Plasmid DNAs were isolated, and an unspliced sequence was obtd. (Q92972) encoding the transmembrane
                                                                                                                                                                                                             Pan Y. Pasternak GW; WPI; 95-193814/25. Pressibly R74298. Pressibly R74298. Nucleic acid molecule(s) encoding a kappa-3 opicid receptor, and antibody against the receptor.
                                                                                                                                                                                                                                                                                                                                                              image cell membrane-bound receptor in a subject
Disclosure; Fig.1; 68pp; English.
Degenerate primers based on conserved sequences of the mouse delt
opioid receptor were used in PCR to amplify mouse kappa-3 opioid
receptor con in a mouse brain lambda ZAP con in 12, 536 A; 680 C; 663 G; 721 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated DNA encoding an opiorph receptor - used to develop prods. for identifying opioid agonists and antagonists and for detection and manipulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T89585 standard; cDNA; 1452 BP.
189585;
12-JAN-1998 (first entry)
Rat orphanin FQ receptor CDNA clone LC132.
Orphanin FQ receptor; binding; locomotor disease; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 25; DB 1; Length 2600;
Pred. No. 0.0061;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 25; DB 1; Length 2706; 100.0%; Pred. No. 0.0061;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                          05-NOV-1993; US-147949.
(SLOK ) SLOAN KETTERING INST CANCER RES.
Pan Y, Pasternak GW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     675 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMCY ) AMERICAN CYANAMID CO.
Eppler CM, Hulmes JD, Ozenberger BA;
WPI; 95-269412/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain opiorph receptor protein 0R7
Sequence 2706 BP; 569 A; 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              597 GACTACTACAACATGTTTACCAGCA 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  677 GACTACTACAACATGTTTACCAGCA 701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-DEC-1995 (first entry)
Rat opiorph receptor OR7 DNA.
Opiorph receptor; opioid; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%;
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Best Local Similarity 100.00
"Thes 25; Conservative
                    299. .1402
/*tag= a
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21-JAN-1994; US-185360.
                                                                                                                                  03-NOV-1994; U12728
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P-PSDB; R76638
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                                                                          WO9512616-A
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092972
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T89585
                       SOCCO SEPTEMBLE SOCCO 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
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DR P-PSDB; R71968.

P-PSDB; R71968.

New nucleic acid encoding new human mu opioid receptor - and practice acid encoding new human secretarial and related vectors, treatment and drug screening.

PT sample 9: Page 218-222; 266pp; English.

CC The CDNA given in 099233 was isolated from a rat brain library by low stringency hybridization with rat un opioid receptor CDNA (Q89222). The clone encoded a 367-amino acid protein (R71968) that showed high homology with mu, kappa and delta opioid receptors but lacked affinity for their ligands, suggesting it to be connence 1567 BP; 313 A; 440 C; 402 G; 412 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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100.0%; Pred. No. 0.0061;
Live 0; Mismatches 0; Indels
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0.0061;
0; Indels
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Rat Opioid receptor CDNA.
Opioid receptor; MOR-1; gene therapy; diagnostic; ss.
Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                      1.8%; Scc. No. v. 100.0%; Pred. No. v. v. v. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            090096 standard; cDNA, 2600 BP.
090096;
03-NOV-first entry)
Mouse kappa-3 opioid receptor.
Kappa-3 opioid receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 173. .1276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               621
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                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
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Best Local Similarity
Matches 25; Conserv
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treatment; opioid inhibitor; opiate induced hypothermia; drug design; KW morphine induced analgesis; methadone specific opioid receptor; ss.

FT Key

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Location/Qualifiers

FT 5/UTR

/*tag= a

182...1285

FT 7

Y*tag= c

NOS707212-A1.

PR 1286..1452

FT 3/UTR

/*tag= c

NOS707212-A1.

PR 12-ANG-1995; US-533058

PR 11-ANG-1995; US-533058

PR 11-ANG-1995; US-533058

NOSM-1995; US-51451.

PR 10-NOV-1995; US-51451.

PR 10-NOV-1995; US-51451.

PR 10-NOV-1995; US-51451.

PR 10-NOV-1995; US-51451.

PR NOSM-NOV-1995; US-51451.

PR NOSM-N
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Db 560 GACTACTACAACATGTTTACCAGCA 584
Search completed: February 17, 2000, 10:11:06
Job time: 1921 sec
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597 GACTACTACAACAIGTTTACCAGCA 621

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0; Gaps

Query Match 1.8%; Score 25; DB 1; Length 1452; Best Local Similarity 100.0%; Pred. No. 0.0061; Matches 25; Conservative 0; Mismatches 0; Indels

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Sequence 3, Appli
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                                                                                                                                                                                                                                                       1410
1 GGGCACCTTGCTGATGCCAA......AAGCCAGATTACAACTGCAG 1410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Number of hits that pass the threshold : 428588

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5D_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/5D_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/FD_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq:*
7: /cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq:*
7: /cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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US-08-1449-093A-3
US-08-141-2494-3
US-08-141-451A-3
US-08-553-058C-3
US-08-544-451A-3
US-08-544-10358-1
PCT-US94-10358-1
PCT-US94-10358-1
PCT-US94-10358-1
PCT-US94-10358-1
US-08-411-859-1
US-08-411-859-1
US-08-204-10358-1
US-08-204-10358-1
US-08-204-10358-1
US-08-204-10358-1
US-08-417-103-111
US-08-417-103-111
US-08-417-103-111
US-08-417-103-111
US-08-417-103-111
US-08-2136-3-1
US-08-142-439A-1
US-08-142-439A-3
US-08-142-439A-3
US-08-36-796-3
US-08-36-796-3
                                                                                                                                                                                                                                                                                                                                                                              214294 seqs, 59861208 residues
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                                                                                           nucleic search, using sw model
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Match Length DB
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                                                                                         nucleic
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<b>488000000000</b>		US/08149  James R David K David K Opioid F SS: E Allegr Wacker Dr NR: E Allegr Wacker Dr NR: Ov-1993 35 WATION: Reviews OWBER: O	1.8%;
1352 21412 21412 2254 11500 11711 11875 11875 11875 11875 11875 11870 11870 11870 11870 11870		Sequence 3, Application US/0814905 Patent No. 565873 Sequence 3, Application US/0814905 Patent No. 565873 GENERAL INFORMATION: David K TITLE OF INVENTION: Opioid Rec NUMBER OF SEQUENCES: ADDRESSEE: Banner & Allegret STREET: 10 South Wacker Driv. CITY: Chicago STATE: Illinois COMPUTR: EADABLE FORM: MEDIUM TYPE: EQOS/MS- SOFTWARE: Patentin Release # COMPUTER: Datentin Release # COMPUTER: 18 PC Compatible OPERATING SYSTEM: PC-DOS/MS- SOFTWARE: Patentin Release # COMPUTER: 16 OF STATE: 05-005/MS- SOFTWARE: Patentin Release # COMPUTER: 16 OF STATE: 05-005/MS- SOFTWARE: Patentin Release # COMPUTER: 18 PS-105/MS- SOFTWARE: Patentin Release # COMPUTER: 18 OF COMPATION: A35 ATTORENT APPLICATION DATA: RELEASTING DATA: RELEASTING SYSTEM: 05-005/MS- TELEPHONE: 312-115-100 TELEFAX: 312-715-1234 TELEPHONE: 312-115-100 TELEFAX: 312-715-1234 TELEPHONE: 312-115-100 TELEFAX: 312-715-1234 TELEFAX: 312-115-1000 TELEFAX: 312-715-1234 TELEFAX: 312-715-12	100
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		1-149-093A- iuence 3, Agent No. 56 APPLICANT: AITLE OF II TITLE OF II TITLE OF II TITLE OF II TITLE OF II CONRESSED SIRET: COUNTRY: ZIP: 60 COUNTRY RA MEDIUM TARESTED COUNTRY RA MEDIUM TARESTED COUNTRY RA MEDIUM TARESTED COUNTRY RA MEDIUM TARESTED ATTORNEY AR APPLICAT FILING CORREDIA SOFTWARE TELECHONIN TEL	. Match Local
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APPLICANT: Grisel, Judith E.
APPLICANT: Grisel, Judith E.
APPLICANT: Grisel, Jeffrey S.
APPLICANT: Mogil, Jeffrey S.
APPLICANT: Mogil, Jeffrey S.
APPLICANT: Mogil, Jeffrey S.
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell Leigh & Whinston LLP STREET: 121 S.W. Salmon, Suite 1600
CITY: Portland
STATE: Oregon
TITLE OF INVENTION: A NO. 5821067el Mammalian Methadone-Specific TITLE OF INVENTION: Opioid Receptor Gene and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
1.8%; Score 25; DB 2; Length 1452;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                             CORRESPONDED ADDRESS:
ADDRESSE: Banner & Allegretti, Itd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: 10 South Wacker Drive, Suite 3000
CITY: 111100is
COUNTRY: 05A
ZIP: 6066
COMPUTER: 11100is
COMPUTER: 11100is
COMPUTER: 1100 Yes: 1000
SPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.25
COMPUTER: 1100 Yes: 1000
SOFTWARE: PATCHIN NOWBER: 05/08/911,245
FILING DATE: 15-NG-1997
CLASSIFICATION NOWBER: 05 00/04-1993
FILING DATE: 06-NOV-1993
FILING DATE: 06-NOV-1993
ATTORNEY/AGENI INFORMATION:
NAME: NO. 5821067nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 39,3311
TELECOMMUNICATION INFORMATION:
TELECOMU
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STRANDEDNESS: single
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                                                              NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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US-08-911-245-3
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US-08-553-058C-3
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KAPPA3 OPIOLD RECEPTORS, RECEPTORS
ENCODED THEREBY, AND USES THEREOF
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              Mismatches
                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pasternak, Gavril W.
APPLICANT: Pan, Ying-Xian
TITLE OF INVENTION: NUCLEIC ACID MOLECT
TITLE OF INVENTION: NUCLEIC ACID MOLECT
TITLE OF INVENTION: NUCLEIC ACID MOLECT
TITLE OF INVENTION: ENCODED THEREBY, AN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
CITY: New York
COUNTRY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/147,949A
FILING DATE: OS-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: White, John P. RECISTRATION WIMBER: 28,678
REPERRENCE/DOCKET NUMBER: 44782/JPW/JKM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 10036
COMPUTER: 10036
COMPUTER: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.30
CURRENT APPLICATION DATA:
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US-08-147-949A-1
'Sequence 1, Application US/08147949A
'Patent No. 5747279
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THEFAX: (212) 391-0525
TELEX: 42253 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2600 base pairs
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Best Local Similarity 100.
Matches 25; Conservative
                 Conservative
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STRANDEDNESS: single
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; LOCATION: 299..1401
; OTHER INFORMATION:
US-08-147-949A-1
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ANTI-SENSE: N
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US-08-911-245-3
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GENERAL INFORMATION:
APPLICANT: DEPLER, C. Mark
APPLICANT: OZENBERGER, BELGEY A.
APPLICANT: OZENBERGER, BELGEY A.
APPLICANT: OZENBERGER, BELGEY D.
TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
TITLE OF INVENTION: TO OPIOID RECEPTORS
INDRESSED: DADDY & DADDY.
STREET: 805 Third Avenue
CITY: New York
STREET: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
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Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 25; Conservative 0; Mismatches 0; Indels
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COMPUTER: ISP PC compatible
COMPUTER: ISP PC compatible
COMPUTER: PatentIR Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FIDICATION NUMBER: US/08/454,549
FILIG DATE: 30-MAY-1995
                                                                                                                                                    FILING DATE: 08/11/95
CLASSIFICATION: 435
PROOF APPLICATION DATA:
PROOF APPLICATION DATA:
APPLICATION NUMBER: 08/553,058
FILING DATE: 11/13/95
ATTONEY/AGENT INFORMATION:
NAME: William D. NO. 5837809nan, M.D.
REGISTRATION NUMBER: 30,878
REGISTRATION NUMBER: 30,878
TELEPHONE: (503) 226-7391
TELEPHONE: (503) 226-7391
TELEPHONE: (503) 226-7391
TELEPHONE: (503) 228-9446
INFORMATION FOR SED ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 base pairs
TYPE: nucleic acid
STARADEDNESS: Single
                                                                                   SOFTWARE: WP5.1 ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/514,451A
FILING DATE: 08/11/95
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WP5.1 ARCTITEL/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     560 GACTACTACACATGTTTACCAGCA 584
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1283..1452
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182..1282
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1..181
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LOCATION:
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US-08-514-451A-3
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1.8%; Score 25; DB 2; Length 1452;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Reinscheid, Rainer K.
APPLICANT: No. 5837809hacker, Hans-Peter
APPLICANT: Monsma, Frederick J.
IIILE OF INVENTION: A NOVEL MAMMALIAN OPIOID
IITLE OF INVENTION: RECEPTOR LIGAND AND USES
CORRESPONDENCE: 16
CORRESPONDENCE ADDRESS:
                                            COMPUTER READALE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: TBM FC competitible
CORNTER: TBM FC competitible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Version WP6, ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,058C
FILING DATE: 11/3/95
CLASSIFICATION NATA:
APPLICATION NUMBER: 514
PRIOR APPLICATION NUMBER: 30,878
FILING DATE:
APPLICATION NUMBER: 30,878
FILING DATE:
APPLICATION NUMBER: 30,974
REGERENCE/DOCKET NUMBER: 30,974
TELECOMMUNICATION NUMBER: 30,974
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 699-40006/WDN
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 699-40006/WDN
TELECOMMUNICATION NUMBER: 6933,226-7391
TELEPROME: 6033,226-7391
TELEPROME: 6033,226-7391
TELEPROME (503) 228-946
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Klarquist Sparkman Campbell ADDRESSEE: Leftgh & Whinston LLP STREET: 121 S.W. Salmon, Suite 1600 CITY: Portland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 597 GACTACTACACATGTTTACCAGCA 621
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Patent No. 5837809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bunzow, James R. APPLICANT: Grandy, David K. APPLICANT: Civelli, Olivier APPLICANT: Reinscheiß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH: 1452 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1283..1452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DESCRIPTION: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5'UTR
1..181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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LOCATION:
FEATURE:
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NAME/KEY:
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US-08-553-058C-3
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US-08-514-451A-3
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            COUNTRY:
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RESULT 8
US-08-411-659-1
; Sequence 1. Application US/08411859
; Patent No. 5985600
; GENERAL INFORMATION:
APPLICANT: EVANS, CHRISTOPHER J.
APPLICANT: EDWARDS, ROBERT H.
TITLE OF INVENTION: EXPRESSION CLONING OF A DELTA OPICID
TITLE OF INVENTION: PRECEPTOR, RELATED EXPRESSION SYSTEMS, AND RELATED
TITLE OF INVENTION: PHARMACEUTICALS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                          1.8%; Score 25; DB 6; Length 1567; 100.0%; Pred. No. 0.0034; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/411,859
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22000-20526.00
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/929,200
FILING DATE: 13-AUG-1992
ATORNEY/AGENT INFORMATION:
NAME: LITHGOM, TIMOTHY J.
REGISTRATION NUMBER: 36,856
REFERENCE/DOCKET NUMBER: 22000-20526
TELECHONE: 415-4813-5600
                                                                                                                                                                                                                                                                                                                                                                          597 GACTACTACAACATGTTTACCAGCA 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        591 TCCATTGACTACTACATGTT 613
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TELERX: 706141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
- "WATH: 1829 base pairs
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
                                                                                                                                                                                                                                                Conservative
; LOCATION: 173..1273 PCT-US94-10358-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29..1144
                                                                                                                                                                       Query Match
Best Local Similarity
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US-08-411-859-1
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                                                                                                                                                                                                                                                    25;
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PCT-US94-10358-16

SQUENCE 16 Application PC/TUS9410358

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: MU OPICID RECEPTORS: COMPOSITIONS AND METHODS

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P. O. Box 4433

CITY: Houston

STREET: P. O. Box 4433

CITY: Houston

STREET: P. O. Box 4433

COUNTRY: USA

ZIP: 77210

COMPUTER: PARABALE FORM:

MEDIUM TYPE: FIOPPy disk

COMPUTER: PATENTN RELEASE #1.0, VERSION #1.25

COMPUTER: PATENTN RELEASE #1.0, VERSION #1.25

COMPUTER: PATENTN RELEASE #1.0, VERSION #1.25

COMPUTER: DATE: CONCURRENT PCT/US94/10368

STILING DATE: OCCURRENT 1084

APPLICATION NUMBER: OS/120.601

FILING DATE: AND RELEASE #1.0, VERSION #1.25

ATTORNEY APPLICATION DATA:

REPERENCE-CAMENT INFORMATION:

RAME: WILLSON, MARK B. 37,259

REPERENCE-COMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMU
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                                            ATTORNEY AGENT INFORMATION:
NAME: ROBINSON, JOSEPH R.
REGISTRATION NUMBER: 33,446
REFERENCE/DOCKET NUMBER: 0646/1A818-US5
TELECOMMUNICATION INFORMATION:
TELEFRAX: (212) 753-6237
TELEFRAX: (212) 753-6237
TELEFRAX: (212) 753-6237
TELERAX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2706 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
SUSSENTINE SUSSENTINE SOURCE:
SUSSENTINE SUSSENTINE SUSSENTINE SOURCE:
SUSSENTINE SUSSEN
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TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 16:
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DENGTH: 1567 base pairs
TYPE: nucleic acid
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                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
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PCT-US94-10358-3
; Sequence 3, Application PC/TUS9410358
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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0
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                                OPERATING SYSTEM: PC_DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358
FILING DATE: CONCURRENTLY herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
1.4%; Score 20; DB 6;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 20; Conservative 0; Mismatches
                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/120.601
FILING DATE: 13 SEPTEMBER 1993
ATOCNET AGENT INFORMATION:
NAME: WILSON, MARK B.
RECISTRATION NUMBER: 37,259
RECISTRATION NUMBER: 37,259
REPERENDE/DOCKET NUMBER: INDAOOSP-TELECOMMUTCATION:
TELECOMMUTCATION INFORMATION:
TELECHONE: (512) 416-3000
TELERAX: (713) 789-2679
TELERAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TILING DATE: CONCURRENTLY herewith CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/120.601
FILING DATE: 13 SEPTEMBER 1993
ATTONNEY, AGENT INFORMATION:
NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKEI NUMBER: 37,259
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
                                                                                                                       Concurrently herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Arnold, White & Durkee STREET: P. O. Box 4433 CITY: Houston
                   IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      700 GIGGACCGCTACATIGCIGT 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            645 GIGGACCGCIACAIIGCIGI 664
                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
214..1410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
                 COMPUTER: IBM PC (OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION:
PCT-US94-10358-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS NUMBER OF SEQUENCES: 17 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM IXPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFIWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/411,859
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 22000-20526.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEPAX: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/929,200
FILING DATE: 13-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Arnold, White & Durkee STREET: P. O. Box 4433
CITY: Houston STRATE: Texas
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US94-10358-1; Sequence 1, Application PC/TUS9410358; GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: LITHGOW, TIMOTHY J. REGISTRATION NUMBER: 36,856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1179 TTTCTGGATGAAAACTTCAA 1198
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COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELLEFAX: 415-494-0792
TELLEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 90 base pairs
TYPE: nucleic acid
SIRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                        CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 20; Conserva
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US-08-411-859-7
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1256 TITCIGGAIGAAAACIICAA 1275

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STRANDEDNESS:
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US-07-816-283-11
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                                                                                    RESULT 13
US-07-816-283-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
WINNERS OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSES: ANDRESS: ADDRESS: ANDRESSES: ANDRESSES: ALOST White & Durkee
STREET: P. O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
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1.4%; Score 20; DB 6; Length 1610;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                         Length 1618;
                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER FALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
SOFTWARE: PATEMIN PC-DOS/MS-DOS/ASCII
SOFTWARE: PATEMIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358
FILING DATE: CONCULTENTLY herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/120.601
FILING DATE: 13 SEPTEMBER 1993
ATFORNEY/AGENT INFORMATION:
NAME: WILSON, MARK B
REGISTRATION NUMBER: 37,259
REFERRENCE/DOCKET NUMBER: INDAOSP--
TELECOMMUNICATION INDERAGION
TELECOMMUNICATION INFORMATION:
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0.99;
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TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1618 base pairs
TYPE: nucleic acid
STRANDEDDESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                700 GEGGACCCCTACATECTCT 719
                                                                                                                                                                                                                                                                                                                                                                                        645 GIGGACCCCIACATIGCIGT 664
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TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 1610 base pairs
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LOCATION:
PCT-US94-10358-3
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-US94-10358-7
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Patent No. 5538882
GENERAL INFORMATION:
APPLICANT: Matsul, Ikuo
APPLICANT: Honda, Kazuhiko
APPLICANT: Honda, Koichi
TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,
TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
TITLE OF INVENTION: Oligosaccharide Using The Enzyme
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blich, Stewart, Kolasch & Birch, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HB: Birch, Stewart, Kolasch & Birch, LLP 8110 Gatehouse Road, Suite 500 East
                                          APPLICANT: Bell, Graeme I.
APPLICANT: Bell, Graeme I.
APPLICANT: Seino, Susumu
APPLICANT: Seino, Susumu
TITLE OF INVENTION: SOMATOSTAIIN RECEPTORS
NUMBER OF SEGURNCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: PO Dox 4433
CITY: Houston
STREET: Toxas
CONTRY: USA
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.2%; Score 17; DB 100.0%; Pred. No. 30; ive 0; Mismatches
Sequence 11, Application US/07816283
Patent No. 5436155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/816
FILING DATE: 19911231
CLASSIPICATION: 435
ATTORREYAGENT INFORMATION:
NAME: McDaniel, C. Steven
TELECOMUNICATION INFORMATION:
TELEPHONE: 713-789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 713-789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1796 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       639 ATGAGTGTGGACCGCTA 655
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Matches 17; Conserve
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DB 1; Length 2061; 30;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,702
FILING DATE: 06 JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                              FILING DATE: 06-UNN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 234-252P TELECOMUNICATION HROPMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8000
TELEFAX: (703) 205-8050
INDORANION FOR SEQ ID NO: 5:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (synthetic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: line
MOLECULE TYPE: I
HYPOTHETICAL: NO
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US-08-470-702-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Library of chromosomal DNA from Bacillus macerans, pMAC, generated by treating chromosomal DNA from Bacillus mad IAMI243 with a restriction enzyme, and inserting and linking restrictio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Nucleotides 1-2061 correspond to nucleotides 82-2142 of the Bacillus macerans cyclomaltodextrin glucanotransferase structural gene"
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VARLANI GENE OF THE ENZYME AND METHOD FOR PRODUCING
OLIGOSACCHARIDE USING THE ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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100.0%; Pred. No. 30;
tive 0; Mismatches 0; Indels
                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/204,656B
FILING DATE: 02-MAR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE TITLE OF INVENTION: VARIANT GENE OF THE ENZING THE TITLE OF INVENTION: OLIGOSACCHARIDE USING THE NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH STEEDE: 8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
                                                                                                                                                                                                                                                    NAME: Weiner, Marc S. REGISTRAINON NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
IELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-08-470-702-5
Sequence 5, Application US/08470702
Patent No. 5631149
GENERAL INFORMATION:
APPLICANT: MATCHI, IKUO
APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: HONDA, KOICHI
APPLICANT: HONDA, KOICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fragments to pBR322
                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (703) 205-8000
TELERA: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 2061 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                FILING DATE: 02-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1.2061

COTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-08-204-6568-9
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Best Local Similarity
Matches 17; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
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em\_est22:\*
em\_est23:\*

gb\_est32:\*

em\_est24:\* em\_est25:\* em\_est26:\*

99\_est33...\*\*

90\_est34...\*\*

90\_est34...\*\*

90\_est34...\*\*

90\_est38...\*\*

90\_est43...\*\*

90\_est43...\*\*

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90\_est44...\*\*

90\_est32...\*\*

90\_est33...\*\*

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February 17, 2000, 09:37:05; Search time 771.69 Seconds (without alignments) 6898.737 Million cell updates/sec
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1410
1 GCGCACCTIGCIGATCCCAA......AACCCAGAITACAACTGCAG 1410
GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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em_est3:*
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gb_est22:*
gb_est23:*
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gb_est24:*
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gb_est27:*
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gb_est29:*
gb_est29:*
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                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
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em\_gss2:\* em\_gss3:\* em\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

gb\_gss12:\*
gb\_gss13:\*
gb\_gss14:\*
gb\_gss15:\*

em\_gss12:\*

925-9885: \*\*
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SUMMARIES

Description	R31984 vh62c10.rt	AW047705 UI-M-BH1-	AA683100 ae81g12.s	AL120154 DKFZp761A	AV387715 AV387715	AW200827 Se94a02.v	AQ674484 HS_5478_B
A		AW047705					
DB.	22	64	37	64	74	74	82
% Query Match Length DB	153	427	303	401	601	509	407
% Query Match	1.8	1.6	1.4	1.4	1.4	1.4	1.4
Score	26	22	20	20	20	20	20
0.	П	7	M	4	വ	9	7
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AQ810283 HS_4786_A A1009309 EST203760 A105468 EST214757 A1256352 uf07a06.x A110541E EST238834 A14110871E EST238834 A14110871E EST238834 A1559367 tn21b12.x A160214 UT.R-AB0-A165932 tuc6b12.x A1659367 tn21b12.x A1659367 tn21b12.x A1679427 tf01003.y B72980 RPCT111-10M2 A0681658 HS_2161_A AQ672191 CITB1-E1-AQ67219 RPCT13-E1-AQ472191 CITB1-E1-AQ67219 RPCT13-E1-AQ67219 RPCT13-E1-AQ67219 RPCT13-E1-AQ67219 RPCT13-E1-AQ67219 RPCT13-E1-AQ67219 RPCT13-E1-AQ67219 RPCT13-E1-AQ67219 RPCT13-E1-AQ67219 RPCT13-E1-AQ67219 RPCT13-E1-AQ6613-E1-E1-AQ67219 RPCT13-E1-AQ67219 RPCT13-E1-AQ67219 RPCT13-E1-AQ67209 RPCT13-E1-AQ67460 RPCT0-E1-E1-AQ6615 EST77582 AAA13015 C10512 C1051 AAA468769 RPCT0-EST77882 AAA17244 ZW920C41 AAA68769 RPCT0-EST77882 AAA17244 ZW920C6.S AAA17244 ZW920C6.S	EST 28-APR-1995 Homo sapiens CDNA clone 5119 MU-TYPE OPIOID RECEPTOR aniata; Vertebrata; Mammalia; Hominidae; Homo. Elliston.K., Hawkins,M., Le.M., Lenon,G., Marra,M., 'I., Soares,M., Tan,F., iamson,A., Wohldmann,P. and Medicine 01, St. Louis, MO 63108
AQ810283 A1009309 A105486 A1105468 A1105468 A1206352 A4410541 A1502174 A1502174 A1502174 A16702174 A16702174 A081658 A081658 A081658 A081658 A0816195 A0812990 A0812990 A0812900 NS731 W09072 NN 78731 W09072 A47218901 A4800300 C15712 C15915 A44686 AA130056 AA130056 AA130056 AA1306290 AA218901 AA36615 AA468760 AA36615 AA468760	ALIGNMENTS  mena  nta Nb2HP Homo  to gb:L25119 M  to gb:L25119 M  rdata; Craniata  arrhin; Homini  Rucaba,T., Le,M  Rollfing,T., Le,M  Rollfing,T., Le,M  Rollfing,T., So,R  R., Williamson  ject  chool of Medici  y, Box 8501, St edu edu  t.ops: 120  m, LLNL
84444444444444444444444444444444444444	53 bp es place similar sequence 7827 7827 7827 158) Cho 158) Cho 1
NW 448 47 12 10 10 10 10 10 10 10 10 10 10 10 10 10	Soares Soares GI:7878 GI:7878 GI:7878 Metazo Metazo Hultmat Hu
	yh62cl0.rl Soares) IMAGE:134322 5'ssi [(HUMAN); mRNA seq R31984. G:781984 R31984. G:78782' EST. human. Homo sapiens Etkaryota; Metazoa Etkaryota; Metazoa Etkaryota; Metazoa Etkaryota; Metazoa Hollan, M. Hultman Parsons, J., Clark; Hiller, L., Clark; Hiller, E., Clark; Hiller, E., Water Wilson, R. Treyaskis, E., Water Treyaskis, E., Water Treyaskis, E., Water Treyaskis, E., Water The WashU-Merck ES' Uppublished (1995) Contact: Wilson RK Washington
88888888888888888888888888888888888888	R31984 Tyb62cli IMAGE11 (HUMAN) FR31984 R31984 R311 R444 R61 R311 R321 R321 R321 R331 R331 R331 R33
0 0 0 0000 0 0 0000 0 0000000000000000	RESULT 1 R31984 LOCUS DEFINITION ACCESSION VERSION VERYWORDS SOURCE SOURCE SOURCE AUTHORS AUTHORS TITLE JOORNAL

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The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the CDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized cerebellum library cDNA Library Preparation: M.B. Scares Lab Clone distribution: NIR BMAP CDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW047705 427 bp mRNA EST 18-SEP-1999 UI-M-BHI-alo-f-04-0-UI.SI NIH_BMAP_M_S2 Mus musculus cDNA clone UI-M-BHI-alo-f-04-0-UI 3', mRNA sequence.

AW047705 AW047705 AW047705 GI:5908234
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 947 Std Error: 0.00 Seq primer: MISRP1 High quality sequence stop: 120. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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97044477
97044477
On Jun 22, 1998 this sequence version replaced gi:3246886.
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
7082-9643, USA
71=1: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
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/note="Wetcor: National State_1: EcoRI; Library constructed from S-11 frontal lobe, male, 34 years old, 50% caucasian, 50% Aleutian. Schizophrenic suicide. Son caucasian, 50% Aleutian. Schizophrenic suicide. Random prinned into EcoRI site of ZAP II Vector. Mass excised. Custom library. Avg insert length 1.4kb. Mass Excised. Custom library. Avg insert length 1.4kb. Mass and the Stanled by Johnston N., Torrey, E.F., Volken R., and the Stanley Neuropathology Consortium - Analysis of RNAs from the Brains of Individuals with Psychiatric Diseases (Unpublished) Stanley Neurovirology Laboratory, Johns Hopkins School of Medicine, Baltimore MD."
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This is the 5' sequence of the clone insert
Clone Irom S. Wiemann, Wolecular Genome Analysis, German Cancer
Research Center (DKTS); Email S. Wiemannédkfez-heidelberg.de;
sequenced by BMFZ within the CDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Frimates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 401)
Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Koehrer, et al.)
Unpublished (1999)
On Feb 18, 1999 this sequence version replaced gi:4297623.
Contact: Koehrer K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
Locatton/Qualifiers
                                                                                                                                                                        /tissue_type="schizophrenic brain S-11 frontal lobe"/dev_stage="34 years old"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MRNA EST 27-SEP-1995 (synonym: hamy2) Homo sapiens CDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.4%; Score 20; DB 37; Length 303; larity 100.0%; Pred. No. 6.8; Conservative 0; Mismatches 0; Indels
                                                                                        /clone="IMAGE:970630"
/clone_lib="Stratagene schizo brain Sll"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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/clone="DkFkp761A137"
/clone_lib="761 (synonym: hamy2)"
/tissue_type="amygdala"
/dev_stage="adult"
/lab_host="DH108"
                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALL20154 401 bp mRNA
DKE2p761A137_r1 761 (synonym: h
DKF2p761A137_5', mRNA sequence.
ALL20154
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                                                                                                                                                    /GD xref="Co-broom"
/GD xref="UI-M-BHI-alo-f-04-0-UI"
/clone="UI-M-BHI-alo-f-04-0-UI"
/clone="UI-M-BHI-BMAP_M-S2"
/dev_stage="27-32 days"
/dev_stage="DHIOB (Life Technologies)"
/lab_nost="PHIOB (Life Technologies)"
/note="Vector: pT713D-pac (Pharmacia) with a modified
polylinker; SIte_1: Not I; Site_2: Sco Ri; The
NH_BMAP_M_S1 library is a subtracted library derived
forlyed from a mixture of normalized libraries from ten
NH_BMAP_M_S1, which in turn is a subtracted library
derived from a mixture of normalized libraries from ten
regions of the mouse brain (cerebellum, brain stems,
olfactory bulbs, hypothalamus, cortex, amygdala, basal
ganglia, pineal gland, striatum, hipoccampus). The driver
used for subtraction consisted of a pool of 5,000 clones
from the NIH_BMAP_M_S1 library and a pool of 5,000 clones
obtained from non-normalized and normalized mouse brain
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Entheria; Primates; Catarrhin; Hominidae; Homo.

Entheria; Naciona; Catarrhin; Hominidae; Homo.

Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.; Schallenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wilie, T., Waterston, R. and Wilson, R. Unpublished (1997)

Entheria; Wilson RK

Washington University School of Medicine

444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Fax: 314, 286, 1810
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Possible reversed clone: similarity no wrong strand
Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 229.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA681100 303 bp mRNA EST 15-DEC-1997 ae81g12.s1 Stratagene schizo brain S11 Homo sapiens CDNA clone IMAGE:970630 3' similar to SW:MAPA_RAT P34926 MICROTUBULE-ASSOCIATED PROTEIN 1A ; mRNA sequence.
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                                                                                                         /organism="Mus musculus"
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TAG_TISSUE=cerebellum
TAG_SEQ=GACTC"
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                                                                                                                                        /strain="C57BL/6J
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Seg primer: M13 Forward POLYA=Yes.
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Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 601)
Asamizu, E., Nakamura, Y., Sato, S., Fukuzawa, H. and Tabata, S.
A Large Scale Structural Analysis of CDNAs in a Unicellular Green
Alga, Chlamydomonas reinhardtii. I. Generation of 3451
non-redundant Expressed Sequence Tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="CM028ell_r"
/clone_lib="Chlamydomonas reinhardtii C9"
/dev_stage="photoautotrophic growth"
/note="Vector: pBluescriptII SR-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                 Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota, Viridiplantee: Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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On Jul 8, 1999 this sequence version replaced gi:5422471.
Contact: Yasukazu Nakamura
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1.4%; Score 20; DB 74; Length 601;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 20; Conservative 0; Mismatches 0; Indels
                                         DB 64; Length 401;
6.8;
                                                                                 Indels
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                                         1.4%; Score 20; DB 100.0%; Pred. No. 6.8 tive 0; Mismatches
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/db_xref="taxon:3055"
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1 (bases 1 to 509)
Shoemaker, R., Kelm, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, C.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
This clone is available through: Galomation
This clone is available through: Galomation
This (800) 433-0030 or (314) 427-3322 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            On Feb 18, 1999 this sequence version replaced gi:4299224. Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1027-387"
/clone_lib="Gm-c1027"
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100.0%; Pred. No. 6.8;
tive 0; Mismatches 0:
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Location/Qualifiers
1. .509
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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequence JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avone North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3618
Fax: (206) 616-3887
Email: jwallacequ, washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Clones may be ourchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 4786 row: I column: 23
Seq primer: I7
Class: BAC ends
High quality sequence stop: 555.
Location/Qualifiers
Ince
   Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases I to 553)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIO09309 398 bp mRNA BST 25-JAN-1999
EST203760 Normalized rat heart, Bento Soares Rattus sp. cDNA clone
RHEBD13 3' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="Plate=4786 Col=23 Row=1" /clone_lib="CIT Approved Human Genomic Sperm Library D" /sex="male"
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                                                                                                                                                          Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
On Feb 19, 1999 this sequence version replaced gi:4143382.
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Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
Kerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog &
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Unpublished (1998)
On Jan 17, 1998 this sequence version replaced gi:2045441.
Contact: Lee, NH
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Exa: (301)-838-0208
Email: nhiee@tigr.org
Seq primer: M13-21.
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Eukaryota, Metazoa, C
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1 (bases 1 to 398)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High Throughput Sequencing Center University of Washington 401 Queen Anne Avonue North, Seattle, WA 98109, USA Tel: (206) 616-3818 Fax: (206) 616-3887 Englishment of Sequencing Center Fax: (205) 616-3887 Englishment of Sequencing Center General Sequencing Center General Sequencing Center General For Englishment of Sequences (Artp://bacpac.med.buffalo.edu). Clones may be purchased from Choter Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 1054 row: N column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 407)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                AQ674484 407 bp DNA GSS 24-JUN-1999 HS_5478_B2_G10_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1054 Col=20 Row=N, genomic survey sequence.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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High quality sequence stop: 407.
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| . 407 | . 407 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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100.0%; Pred. No. 6.8;
Live 0; Mismatches 0; Indels
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Mismatches
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                                                                                                                                                                                                                                               AQ674484.1 GI;5207230
229 TTCITGGCCTTTTGGAGATG 210
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AL226352 890 bp mRNA EST 29-OCT-1998 uf07a06.yl Soares mouse mammary gland NMLMG Mus musculus cDNA clone. INAGE:1510642 5' similar to SW:ARG2_MOUSE 008691 ARGINASE II AL226352
                                                                                                                                                                                                                                 AI105468 447 bp mRNA EST 20-JAN-1999
EST214757 Normalized rat Kidney, Bento Soares Rattus sp. cDNA clone
RKIBK02 3' end, mRNA sequence.
AI106468.1 GI:3709542
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Lee,N.H.; Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J., Kerlavage,A.R. and Adams,M.D.
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100.0%; Pred. No. 24;
iive 0; Mismatches 0; Indels
                                            Length 443;
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                                                                                                                  777 GGCACCAAAGICAGGGAAG 795
                                                                                                                                                152 gecaccaaagreaggaag 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1998)
Other ESTS: TC53042
Contact: Lee, NH
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                                                 Query Match 1.33
Best Local Similarity 100.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
NGI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
(CGAP/BTGAP), Tumor Gene Index
Unpublished (1988)
On Sep 12, 1996 this sequence version replaced gi:1404573.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@inh.gov
Tissue Procurement: David N. Louis, Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                       AI056367 443 bp mRNA EST 24-SEP-1998 oy48006.xl NCI_CGAP_Brn23 Homo sapiens CDNA clone IMAGE:1669066 3', mRNA sequence.
AI056367 I GI:3330233
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Seq primer: -40ml3 fwd. ET from Amersham.
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The Institute for Genomic Research
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Matches 19; Conservative
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Best Local Similarity
Matches 19; Conserv
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jote—"Vector: pr773D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - Oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr773 vector. Library is normalized. Library was constructed by Bento Scares and M. Fatima Bonaldo."
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                                            Dubuque, I.,
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1 (bases 1 to 452)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
Gene Index
Unpublished (1998)
On Apr 7, 1998 this sequence version replaced gi:3034510.
ATCC
                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:397494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
               1 (bases 1 to 890)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuc Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theissing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                               Unpublished (1996)
On Jan 199 this sequence version replaced gi:2286647.
Contact: Marra M/Mouse EST Project
Washington University School of Medicinep
H44 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:1510642"
/clone=lib="Soares mommary gland NMLMG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43; Length 890;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
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Pred. No. 24;
0; Mismatches
                                                                                                                                              The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                          Seg primer: -40RP from Gibco
High quality sequence stop: 405.
Location/Qualifiers
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Lee, N. H., Glodek, A., Chandra, I., Mason, T. M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                         Gaps
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Vector: pT7T3Pac; Site_1: EcoRI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1998)
On Apr 7, 1998 this sequence version replaced gi:3034844.
Contact: Lee, NH
AICC
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9712, Medical Center Drive, Rockville, MD 20850, USA Tel: (301)-838-329
Fax: (301)-838-0208
Email: nhlee@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                            46; Length 452;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, Tel: (301)-838-3529 Fax: (301)-838-0208
Email: nhlee@tigr.org
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24;
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100.0%; Pred. No. 24;
ative 0; Mismatches
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/organism="Rattus sp."
/b_xref="taxon:10118"
/clone="RHECX48"
/clone=lib="Normalized refore="organ: heart; vect site_2: Not!"
a 107 c 128 g 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.3%; Score 19;
100.0%; Pred. No.
ative 0; Mismatch
                                                                                                                                    /organism="Rattus sp."
/db_xref="taxon:10118"
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AI410875.1 GI:4254379
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us-08-455-683-1.feb17oligo.rst

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1. .233
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                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 233)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index

In Onpublished (1998)

On Jun 5, 1998 this sequence version replaced gi:3189024.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert Strausbergenih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. Clone distribution: Washington University Genome Sequencing Center Clone distribution: N.C.GAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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                                                                           AIS59367 233 bp mRNA EST 12-MAY-1999
tn2lb12.xl NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2168255 3',
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Best Local Similarity 100.
Matches 19; Conservative
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AI559367
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Search completed: February 17, 2000, 09:50:15 Job time: 790 sec

	(ME)
1	<u>}</u>

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

MasPar time 23.72 Seconds 340.625 Million cell updates/sec Thu Feb 17 11:11:36 2000;

not generated. Tabular output

Run on:

Description: Perfect Score:

>US-08-455-683-2 (1-380) from USO8455683.pep 2839 1 MESPIQIFRGDPGPICSPSA......RNTVQDPASWRDVGGMNKPV 380

Sequence:

PAM 150 Gap 11 Scoring table:

170751 seqs, 21266608 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq35

Mean 35.005; Variance 158.855; scale 0.220 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		о¥		SUMMARIES		
Result		Query				4.4
No.	Score	Match	Length DB	a db	Description	Pred. No.
	2839	100.0			use kappa	7.338-252
2	83	100.0	380 34	W44939	kappa opiate r	
æ	2829	9.66	380 14		oiate re	6.49e-251
4	2823		т	F R72591	Mammalian kappa opioi	2.40e-250
S	2746	7.96	380 27		Н	4.66e-243
9	2746	96.7	Н	7 R88722	opioid r	4.66e-243
7	2737	96.4	C.1			3.31e-242
∞	2559	90.1	C/I	7 W30299		2.29e-225
σ	2130	Ŋ.	Н	R67	kappa opioid r	.59e-18
10	1683	59.3	356 11	L R65188	ubtype o	7
11	1678	59.1	398 34	W44937	Mouse mu opiate recep	14
12	1677	59.1	Н	3 R71966	Human mu opioid recep	3.44e-142
13	67	59.0	398 I4	R767		4.27e-142
14	9	59.0	398 13			4
15	1675	59.0	400 14		Human mu opiate recep	5.30e-142
16	1610	56.7	372 14	1 R76782	Rat delta opiate rece	113

380 AA;

Sequence

.12e-13	1.12e-134	.12e-13	.76e-12	.81e-12	.40e-12	.35e-12	.51e-12	.51e-12	.51e-12	.77e-9	.77e-7	.12e-7	.13e-7	.49e-7	.49e-7	.88e-7	.09e-6	.62e-6	.52e-6	.59e-6	.13e-5	.68e-5	.63e-4	.39e-4	.39e-4	.39e-4	.47e-4	Le-4	
e of murine d	use delta opioid	e delta opiate r	ine delta opioid	id recepto	se opioid rece	at opiorph recepto	at methadone-specif	methadone-	t orphanîn FQ_rec	appa-3 opioid	Murine somatostatin z	Human somatostatin re	ostatin	Human somatostatin re	uman somatostatin r	tary somatostat	silon opioid recep	at RGH G-protein co	HJP G-protein	n somatostatin r	lon opioid recep	rine somatostati	rotein coupled r	MIP-1 alpha/	kine recep	-lalp	at galanin recepto	GalR	
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## ALIGNMENTS

Polynucleotides and peptides derived from opioid receptor
Polynucleotides and peptides derived from opioid receptor
Polynucleotides for use in therapeutic compositions and in
Polynucleotides for useful drug substances.

Screening assays for useful drug substances.
Claim 8; Page 207-211; 300pp; English.

Claim 8; Page 207-211; 300pp; English.

Claim 8; Page 207-211; Bollish in English.

Claim 8; Page 207-211; Bollish in English.

Claim 8; Page 207-211; Bollish in English in Englis R67669; 17-A0G-1995 (first entry) Mouse kappa opioid receptor mORKI. Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify; transmembrane domain; somatostatin; receptor; human; expression vector; truncate; chimaeric; assay; probe. Mus musculus. MOSTAL 1994. 20-MAY-1994; U05747. 20-MAY-1993; US-066296. 30-JUL-1993; US-147592. (ARRH-) ARCH DEV CORP. (ARRH-) ARCH DEV CORP. MPI; 95-022804/03. RESULT 1 ID R67669 standard; Protein; 380 AA. N-PSDB; Q75926 WO9428132-A. NAME DO PARA DE PARA D

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This sequence represents the mouse kappa opiate receptor. The gene sequence is used to generate a transgenic non-human mammal for identifying agents for treating disorders associated with opiate receptors. In the mammal, the expression of the gene encoding the opiate receptor is modified, particularly by the deletion of an exon and/or insertion of a marker gene, e.g. the neomycin resistance gene, into the sequence. Especially the expression of the gene is altered in nervous tissue. The agents are potentially useful for treating severe pain (chronic or acute), drug addiction and/or prevention or treatment of transplant rejection (as immunosuppressents). The method may isolate and identify powerful analgesics that lack morphine-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse; kappa opiate receptor; transgenic animal; mammal; identification; exon; nervous tissue; pain; drug addiction; transplant rejection; immunosuppressant; analgesic; morphine; side effect.
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                                                                                                        61 iitavysvvfvvglvgnslvmfviirytkmktatniyifnlaladalvtttmpfgsavyl 120
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Length 380;
                           Indels
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Pred. No. 7.33e-252;
 Score 2839; DB 13;
Pred. No. 7.33e-252;
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11-JUL-1997; F0.1282.
15-JUL-1996; FR-008810.
15-JUL-1996; FR-008810.
Dierich A, Kieffer BL, LeMeur M, Matthes HWD,
WPI; 98-110582/10.
                             0; Mismatches
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28-007-1998 (first entry)
Mouse kappa opiate receptor;
exon; nervous tissue; pain; dry
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W44939 standard; Protein; 380
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llarity 100.0%;
Conservative
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Best Local Similarity 100.0%;
Matches 380; Conservative
    Query Match
Best Local Similarity
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W09802534-A2.
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WPI; 95-275452/36.

New DNA encoding human mu opiate receptor - used esp. for screening ords. for activity as opiate agonists or antagonists or activity as opiate agonists or antagonists or activity as opiate agonists.

NMOR CDNA was obtd. from a human cerebral cortical cDNA library screened with fragments of a rat mu opiate receptor. The encoded protein showed homology to rat mu, delta and kappa opiate receptors (R76781-83).
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mnswpfgdvlckivisidyynmftsiftltmmsvdryiavchpvkaldfrtplkakiini
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                                                                   iitavysvvfvvglvgnslvmfviirytkmktatniyifnlaladalvtttmpfqsavyl
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Kappa opiate receptor; mu optiate receptor; hMOR; opiate agonist;
opiate antagonist; drug abuse; analgesic.
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Pred. No. 6.49e-251;
3; Mismatches 1;
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R76783 standard; Protein; 380
R76783;
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larity 98.9%;
Conservative
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30-JAN-1995; U01144.
28-JAN-1994; US-188275.
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Best Local Similarity
Matches 376; Conserv
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W09520667-A1.
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STSHSTAALSSYYFCIALGYTNSSLNPVLYAFLDENFKRCFRDFCFFIKMRMEROSTNRV 360
     14-APR/1998 (first entry)
Human kappa opioid receptor.
Selective target cell activation; G protein-coupled receptor;
RASSL; gene therapy, cell proliferation; kappa opioid receptor;
human; transgenic animal; arrhythmia; bone disease; seizure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "potential N-glycosylation"
39
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/note= "transmembrane"
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/label= N-terminus
/note= "extracellular"
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/note= "transmembrane"
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/note= "transmembrane"
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/note= "extracellular"
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/note= "transmembrane"
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/note= "Extracellular"
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/note= "Extracellular"
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'note= "transmembrane"
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'note= "Cytoplasmic"
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/note= "cytoplasmic"
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W30297 standard; Protein; 380 AA.
W30297;
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The amino acid sequence of the novel mammalian kappa opioid receptor.

The gene was isolated by amplifying a fragment from rat brain mRNA by reverse transcriptase-PCR (RTOFN using primers 086726-7 derived from the mouse delta-opioid receptor gene. This fragment was cloned into the plasmid pCRII to produce pRII. The plasmid pRII was used to probe a rat brain DNA library in lambda ZAPII to obtain a clone of the rat kappa opioid receptor gene, designatd pKOPR2. This clone was introduced into E.coli JM109 for production of the receptor protein. The receptor protein is useful. If a screening of analgesic and hypnotic compounds including
                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-1995 (first entry)
Mammalian kappa opioid receptor protein.
Mammalian kappa opioid receptor; mouse delta opioid receptor; analgesic; amplification; primer; rat; probe; E.coli; RI-PCR; hypnotic compound; ds. Rattus rattus.
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Pred. No. 2.40e-250;
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/product= kappa opioid receptor
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09-JUL-1993; JP-170591.
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N-PSDB; Q86725.
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Selective activation of target cell expressing modified G protein coupled receptor - allows control of cellular proliferation, respecially for amplification of transfected cells in gene therapy.

This protein comprises human kappa opioid receptor (KOR), a protein-coupled receptor implicated in neurotransmission. A novel method for selectively activating a target cell (TC) comprises: (1) introducing into the cell a nucleic acid sequence (1) that expresses a G protein-coupled receptor (A) modified to be activated superiorly by a synthetic ligand (RASIL); and (ii) exposing the transfected cell to small synthetic molecules (B) that bind to and activate (A), inducing the G protein coupled cellular capposing the transfected cell to small synthetic molecules (B) that bind to and activate (A), inducing the G protein coupled cellular capponse associated with receptor activation. (A) has: (a) decreased binding affinity for a selected natural ligand of the native receptor; (b) binding affinity for (B); and (c) is activated by binding (B) sufficiently to produce the required cellular response. Also new are: (1) transgenic cells including neterologus (I) in the genome: (2) cellular implants comprising a con-human animals expressing (A). Activation of (A) transgenic cellular product, particularly a heterologous therapeutic protein encoded by a second inserted nucleic acid sequence. Particularly transfected during gene therapy procedures. Other responses that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transfected during gene therapy procedures. Other responses that can be regulated are cell migration and contraction, or pigment production. In transgenic animals, expression or stimulation of (A) is designed to develop cardiac arrhythmia, symptoms of bone disease, seizures, vascular contractions, dementia, neurodegeneration etc. for use as models of these diseases (claimed). The transgenic
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Pred. No. 4.66e-243;
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||||||||| :||: ||||||
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ilarity 93.7%;
Conservative
                            26-MAR-1996; US-622348.
(REGC ) UNIV CALIFORNIA.
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Best Local Similarity 9
                                                                                                        WPI; 97-502739/46.
N-PSDB; T90998.
                                                                                    Conklin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --1
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                                                                                              Human kappa opioid receptor.
Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
neurology; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Page 13-15; 30pp; French.
The sequence coding for the human kappa opioid receptor was obtained from two overlapping CDNA fragments isolated from a human placental CDNA library. The fragments were amplified from the library using PCR primers based on the sequence of human penentic clones which hybridised with a murine delta receptor oppose. Nucleotide probes derived from the kappa opioid receptor coding sequence are useful for diagnosis of neurological, eachor receptors. The receptor can be used for identifying e.g. agonists of its activity for potential use as analgesics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 mdspiqifrgepgptcapsaclppnssawfpgwaepdsngsagsedaglepahispaipv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MESPIQIFRGDPGPTCSPSACLLPNSSSWFPNWAESDSNGSVGSEDQQLESAHISPAIPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              iitavysvvfvvglvgnslvmfviirytkmktatniyifnlaladalvtttmpfqstvyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ilivcytlmilr1ksvr11sgsrekdrn1rritr1v1vvvavfvvcwtpihifi1vealg
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                                                                                                                                                                                                                                                                                                                                                                                    human Kappa opioid receptor - usefu
for isolating receptor ligands and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 380;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2746; DB 17;
Pred. No. 4.66e-243;
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Human kappa opioid receptor fusion polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Mismatches
                                                                                                                                                                                                                                                                   11-JUL-1994; FR-008531.
(UYST-) UNIV PASTEUR STRASBOURG LOUIS.
Kieffer B, Simonin F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
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W30298 standard; Protein; 427
W30298;
T 6
R88722 standard; Protein; 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rntvqdpaylrdidgmnkpv 380
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                                                                                                                                                                                                                                                                                                               Kieffer B, Simonin F;
WPI: 96-097628/10.
N-PSDB, T12550.
New nucleic acid encoding thin diagnosis and therapy, an
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Local Similarity 93.7%;
nes 356; Conservative
                                                                       (first entry)
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Selective target cell activation; G protein-coupled receptor; RASSL; gene therapy; cell proliferation; kappa opioid receptor; human; transgenic animal; arrhythmia; bone disease; seizure; vascular contraction; disease model.
                                                                                                                   /note= "human kappa opioid receptor"
                                                          1..30
/label= Sig_peptide
/note= "prolactin signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "potential N-glycosylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "potential N-glycosylation"
                                                                                                                                          /note-
96.122
/label= IMH1
/+o= "transmembrane"
                                                                                                                                                                                                                             .55.....
/label= E2
^~~+^= "Extracellular"
                                                                                                                                                                                                                                                                                                                                                                                                      /label= TMH6
/note= "Transmembrane"
337..348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "transmembrane"
                                                                                                                                                                                                       /label= IMH2
/note= "transmembrane"
.55..169
                                                                                                                                                                                                                                                                                                                                                                                                                                /label= E3
/note= "Extracellular"
349..370
                                                                                                                                                                                                                                                                                                                                                            'label= TMH5
'note= "transmembrane"
                                                                                                                                                                                                                                                                  'note= "transmembrane"
                                                                                                                                                                                                                                                                                                           /label= TMH4
/note= "transmembrane"
                                                                                                                                                                                                                                                                                                                                          'note= "extracellular"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= C-terminus
/note= "cytoplasmic"
                                                                                                                                                                                  /label= i1
/note= "cytoplasmic"
                                                                                                                                                                                                                                                                                                                                                                                         'note= "Cytoplasmic"
                                                                                                                                                                                                                                                                                          'note= "Cytoplasmic"
                                                  Location/Qualifiers
                                                                                                                          19..95
/label= N-terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "palmitate"
418..427
/label= HA
                                                                                  31..38
/label= FLAG
                                                                                                                                                                                                                                                           'label= TMH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= TMH7
                                                                                                 39..417
/label= KOR
                                                                                                                                                                                                                                                                                                                           234..259
/label= E2
                                                                                                                                                                                                                                                                                    /label= 12
                                                                                                                                                                                                                                                                                                                                                                                    'label= I3
                                                                                                                                                                                                  154
                                                                                                                                                                                                                                                                                                                                                    .284
                                                                                                                                                                                                                                                                                                                                                                            .312
                                                                                                                                                                                                                                                                                                                                                                                                   .336
                                                                                                                                                                                                                                                                                                                                                                                                                            .348
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                                                                                                                                                                                                                                                                                                   .233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68..247
                                   Chimeric - Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-OCT-1997,
25-MAR-1997; U05334.
26-MAR-1996; US-622348.
                                          Chimeric - Synthetic.
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Modified_site
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Selective activation of target cell expressing modified 6 protein coupled receptor - allows control of cellular proliferation.

Symple 1, Page 77.79; ILTPP; English.

This polypeptide comprises the human G protein-coupled kappa opioid receptor (KOR) (see also W30.297) flanked by N.- and C-terminal sequences that facilitate the detection and C-terminal sequence (I) introducing into the cell a nucleic acid sequence (I) that expresses a RASEL (A) and (1) exposing the transferted cell to small synthetic molecules (B) that bind to and activate (A), inducing the G protein coupled cellular response transferted cell to small synthetic molecules (B) that bind to and activate (A), inducing the G protein coupled cellular response. Also new are: transgenic cells including heterologous (I) in the genome; cellular implants comprising a TC transfered by binding (B) sificiently to produce the required cellular response. Also new are: transgenic cells including heterologous (I) in the genome; cellular implants comprising a TC transfercted with (I); isolated (I); and transgenic animals expressing (A). Activation of (A) results in vitro or in vivo, in cellular proliferation, or secretion of a cellular product, particularly than sfected during gene therapy content are successfully transferted during gene therapy content and contraction, or pigment production. In transgenic animals, expression or stimulation of (A) is designed to expense callurant production of the callular profiles and contraction of the callular profiles and contraction of the callular profiles and contraction of sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiac arrhythmia, symptoms of bone disease, seizures, vascular contractions, dementia, neurodegeneration etc., for use as models of these diseases (claimed). The transgenic animals are also used for production of improved food products (e.g. increased calcium content in eggshells or altered fat/lean ratios) or to control fertility or induce labour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vdspiqifrgepgptcapsaclppnssawfpgwaepdsngsagsedaqlepahispaipv
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Pred. No. 3.31e-242;
19; Mismatches 6; Indels 0;
                                                                                            Selective activation of target cell expressing modified G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rntvqdpaylrdidgmnkpv 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 93.4%;
Matches 355; Conservative
(REGC ) UNIV CALIFORNIA.
Conklin BR;
                                               WPI; 97-502739/46.
N-PSDB; T90999.
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                                                                           Human kappa opioid receptor RASSL ORI.
Selective target cell activation; G protein-coupled receptor;
RASSL; gene therapy; cell proliferation; kappa opioid receptor;
human; transgenic animal; arrhythmia; bone disease; seizure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "extracellular, contains 17 amino acid
residues from delta opiod receptor
(Val-235, Gln-237, Pro-238, Asp-240,
Gly-241, Ala-242, Val-243, Val-244,
Thr-246, Ser-251, Pro-252, Ser-253,
Trp-254, Tyr-255, Thr-258, Val-259,
Thr-260)"
                                                                                                                                                                                                                                                                                                                 'note= "human kappa opioid receptor"
                                                                                                                                                                                                    346..367
/label= TMH7
/note= "transmembrane"
368.414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           //abel= TMH4
/note= "transmembrane"
                                                                                                                                                                                                                                                                                                                            9..95
/label= N-terminus
/note= "extracellular"
                                                                                                                                                                                                                                                                                                                                                                                                           "transmembrane"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "transmembrane"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55..169
|Tabel= E2
|note= "Extracellular"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label= TMH3
note= "transmembrane"
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/note= "transmembrane"
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'note= "Transmembrane"
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/label= E3
/note= "Extracellular"
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/note= "cytoplasmic"
168..245
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'note= "Cytoplasmic"
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                                                                                                                                         vascular contraction; disease model
Chimeric - Homo sapiens.
Chimeric - Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "cytoplasmic'
                                                                                                                                                                                       Location/Qualifiers
              M. 8
W30299 standard; Protein; 424 AA.
                                                                                                                                                                                                                                                                                                                                                                        96..122
/label= TMH1
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                                                                                                                                                                                                                                                                                  39..414
/label= KOR
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/label= E2
                                               W30299;
14-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        label= Il
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133..154
/label= T
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/label= I
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                  RESULT
                                               PARTICICATOR CONTRACTOR CONTRACTO
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Particular activation of target cell expressing modelized & protein coupled receptor - allows control of cellular proliferation, especially for amplification of transfected cells in gene therapy expecially for amplification of transfected cells in gene therapy coupled transports of a contract of special comprises RASI Call, a G protein-coupled receptor (ROR) (see also WAD27) modified at 17 amino acid poloid receptor (ROR) (see also WAD27) modified at 17 amino acid poloid receptor (ROR) (see also WAD27) modified at 17 amino acid poloid receptor (ROR) (see also WAD27) modified at 17 amino acid poloid receptor (ROR) (see also WAD27) modified at 17 amino acid poloid receptor (ROR) (see also WAD27) modification of recombinant protein. A novel method for selectively cativating a target cell (TO) comprises: (1) introducing into the cativating a target cell (TO) comprises: (1) introducing into the cell a nucleic acid sequence (T) (see T9260) that expresses RASIC (B) that bind or and activate (A), inducing the 6 protein coupled cellular response associated with receptor activation. (A) has: (a) decreased binding affinity for a selected natural ligand of the callular implants comprising a TC transfected with (I); in the decreased binding affinity for gloid cellular response (C) is and transferic cells including affinity for (B); and (C) is activation of a cellular implants comprising a TC transfected with (I); isolated (I); and transgenic animals expressing (A). Activation of secretion of a cellular product, particularly a heterologous cold cellular product, particularly a heterologous cold cellular product on the response therapeutic protein encoded by a second inserted nucleic acid sequence. Particularly it is used to expand the relatively few cells that are successfully transfected during gene therapy contraction, or pagenty production of acid mals, expression or stimulation of (A) is designed to develop candar arrhythmia, symptoms of bone diseases, salures, weached contraction, or pigment production of included for p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Selective activation of target cell expressing modified G protein
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Pred. No. 2.29e-225;
20; Mismatches 16; Indels 5
                                     'note= "potential N-glycosylation"
                                                                                                         'note= "potential N-glycosylation"
                                                                                                                                                                         /note= "palmitate"
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Best Local Similarity 89.2%;
Matches 340; Conservative
                                                                                                                                                                                                                  415..424 /
/label= HA
                                                                                                                                                                                                                                                                                                                                                                                            26-WAR-1996; US-622348.
(REGC) UNIV CALIFORNIA.
CONKLID BR:
WPI: 97-502739/46.
N-PSDB: T92601.
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25-MAR-1997; U05334.
Modified_site
                                                                       Modified_site
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Location/Qualifiers
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Sequence 356 AA;
                                                                                                                                                                                                                                                                                                                      for protein kinase
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                                                                                                                                                                      AA.
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R65188 standard, Protein, 356
R65188,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMCY) AMERICAN CYANAMID CO.
Corbett MJ, Eppler CM, Shie
WPI; 94-265963/33.
N-PSDB; Q79199.
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Conservative
                                                                                                                                                                                           19-APR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "h
236..257
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274..294
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26-FEB-1993; US-026
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                                                                                                                                                                                                                                     Rattus rattus
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Best Local S:
Matches 213
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Claim 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymuclectides and peptides derived from opioid receptor
Polymperides - for use in therapeutic compositions and in
screening assays for useful drug substances.
Scham 12; Page 236-239; 300pp; English.
Contactual amino acid sequence of the novel human kappa opioid receptor.
Conte correspoding gene was isolated from a human brain hippocompus CDNA
Ilbrary using a probe from the mouse kappa opioid receptor gene (075926).
Contactual smissing the N-terminal sequence. The C-terminal sequence is
Conteminal 293 amino acids, 281 residues are identical and 6 residues
Conteminal 293 amino acids, 281 residues are identical and 6 residues
Conteminal 293 amino acids, 281 residues are identical and 6 residues
Conteminal 293 amino acids, 281 residues are identical and 6 residues
Conteminal 293 amino acids, 281 residues are identical and 6 residues
Conteminal 293 amino acids, 281 residues are identical and 6 residues
Conteminal 293 amino acids, 281 residues are identical and 6 residues
Conteminal 293 amino acids, 281 residues are identical acceptor for produced are useful for the development of novel assays designed to select or improve substances,
Compable of interacting with the opioid receptor proteins, for use in
Conteminal 295 AA;
Sequence 295 AA;
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                                                                                                                                                                                                                  18-AGG-1995 (first entry)
Human kappa opioid receptor partial protein.
Mouse: kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify; transmembrane domain; somatostatin; receptor; human; expression vector;
 274 liiivoytlmilrlksvrllsgsrekdrnlrritrlvlvvvavfvvcwtpihifilveal 333
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                                                                     300 GSISHSTAALSSYYFCIALGYTNSSINPVLYAFLDENFRRCFRDFCFPIKWRMERQSTNR
              gstshstaalssyyfcialgytnsslnpilyafldenfkrcfrdfcfplkmrmergstsr
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Pred. No. 7.59e-185;
13; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                            /label= Any amino acid
269
                                                                                                                                                                                                                                                                                                                                label= Any amino acid
                                                                                                                                                                                                                                                                                                                                                            abel= Any amino acid
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                                                                                                                                                                                                                                                                           chimaeric; assay; probe.
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R67672 standard; Protein; 295 AA.
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                                                                                                          vrntvqdpaylrdidgmnkpv 414
                                                                                                                                      360 VRNTVQDPASMRDVGGMNKPV 380
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Local Similarity 92.5%;
Nes 273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          08-DEC-1994; 005747.
20-MAY-1994; U05747.
20-MAY-1993; US-066296.
30-JUL-1993; US-100694.
05-NOV-1993; US-147592.
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Bell GI, Reisine I,
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N-PSDB; Q75931.
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                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                          394
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207 VIECSLQFPDDEXSWWDLFMKICVFVFAFVIPVLIIIVCYILMILRLKSVRLLSGSREKD
                                                                                                                                            267 RNLRRITKLVLVVVAVFIICWTPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLN
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                                                                                                                                                                                                                                'note= "Threonine residue especially favourable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Fig 9; 39pp; English.

R65188 is the rat mu-subtype opioid receptor protein purified from rat brain membranes, with biotinyl.b-endorphin (R56665) as its ligand. It is encoded by the nucleotide sequence 079199 which was synthesised using 071022 and 071023 as PCR primers. R65188 is useful for identifying othe receptor subtypes, for screening new opioid ligands, and for studying mechanisms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pure mu-type opioid receptor protein - and nucleic acid coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10..12 / ____/note= "Putative N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "hydrophobic membrane spanning region"
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Mu-subtype opicid receptor; MSOR; drug addiction.
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Pred. No. 9.39e-143;
60; Mismatches 62;
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ce= "hydrophobic membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transgenic animals defective in one type of opioid receptor - used transgenic animals defective in one type of opioid receptor - used transgenic animals for treatment of pain, drug addiction and transgenic presents for treating side effects of known opiate(s) bisclosure; Fig II: 58pp; French.

This sequence represents the mouse mu opiate receptor. The gene sequence is used to generate a transgenic non-human mammal, for identifying agents for treating disorders associated with opiate receptor: In the mammal, the expression of the gene encoding the opiate receptor is modified, particularly by the deletion of an exon and/or insertion of a marker gene, e.g. the neomyclin resistance gene, into the sequence. Especially the expression of the gene is altered in nervous tissue. The agents potentially useful for treating severe pain (chronic or acute), drug addiction and/or prevention or treatment of transplant rejection (as immunosuppressants). The method may isolate and identify powerful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .,
                                                                                                      275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse, mu opiate receptor; transgenic animal; mammal; identification; exon; nervous tissue; pain; drug addiction; transplant rejection; immunosuppressant; analgesic; morphine; side effect.
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                                                    181 hptw-ywenllkicvfifafimpvliitvcyglmilrlksvrmlsgskekdrnlrritrm
                                                                                                                                                           240 vlvvvavfivcwtpihiyviikalitipettfqtvswhfcialgytnsclnpylyaflde
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUL-1997; F01282.
15-JUL-1996; FR-008810.
(CNRS ) CENT NAT RECH SCI.
OLICICA A, Kieffer BL, LeMeur M, Matthes HWD, Simonin FH;
WPI; 98-110582/10.
N-PSDB; V49252.
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55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         W44937 standard; Protein; 398 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse mu opiate receptor.
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es 208; Conser
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WO9802534-A2.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   claim 4; Page 211-214; 266pp; English.
A cDNA library constructed from human caudate nucleus mRNA was screened with rat mu opicid receptor cDNA under conditions of low stringency. One positive clone included the sequence given Q89226, encoding a mu opicid receptor MOR (R71964). The cDNA is used for prodn. of recombinant MOR, in gene therapy, etc.
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Mu opiate receptor; hMOR; opiate agonist; opiate antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding new human mu opioid receptor - and related vectors, transformed cells, antibodies etc., useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                     Human mu opioid receptor.
Mu opioid receptor; MOR; gene therapy; diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1677; DB 13;
Pred. No. 3.44e-142;
52; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis, treatment and drug screening.
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30-0AN-1995; U01144.
28-JAN-1994; US-188275.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                               AA.
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                                                                        7T 12
R71966 standard; Protein; 400 ;
R71966;
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Local Similarity 66.6%;
Les 207; Conservative
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13-SEP-1994; U10358.
13-SEP-1993; US-120601.
(INDV ) UNIV INDIANA FOUND.
                                                                                                                                              (first entry)
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R76781;
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Rattus sp.
W09520667-A1.
RVR-NTVQDPASMRDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         400 AA;
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N-PSDB; 089226
                                                                                                                                                                                                                       Homo sapiens
WO9507983-A.
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                                                                                                        screening
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New nucleic acid encoding new human mu opioid receptor - and related vectors, transformed cells, antibodies etc., useful in diagnosis, treatment and drug screening.

Disclosure, Page 190-194; 266pp; English.

A 365 bp fragment of the mouse delta opioid receptor was used to screen a rat brain cDNA library under low stringency conditions.

One positive clone included the sequence given in 089222, encoding transfected CHO cells.
                                                                                                                  cpds. for activity as opiate agonists or antagonists bisclosure; Page 26-28, 49pp; English.

MAGR CDNA was obtd. from a human cerebral cortical cDNA library screened with fragments of a rat mu opiate receptor. The encoded protein showed homology to rat mu, delta and kappa opiate secuence (R76781-83).
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Pred. No. 6.58e-142;
54; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                             Score 1676; DB 14; Length 39
Pred. No. 4.27e-142;
53; Mismatches 50; Indels
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Rat mu opioid receptor.
Mu opioid receptor; MOR-1; gene therapy; diagnostic.
Wattus sp.
W09507983-A.
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DEPT HEALTH.
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R71964;
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Best Local Similarity 65.8%;
Matches 208; Conservative
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13-SEP-1994; U10358.
13-SEP-1993; US-120601.
(INDV ) UNIV INDIANA FOUND.
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Best Local Similarity 66.18;
Matches 209; Conservative
                  (USSH ) US SEC DEPT HEALT
Johnson PS, Persico AM,
WPI; 95-275452/36.
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                                                                            nvcnwilssaiglpvmfmattkyrqg-s-idctltfshptw-ywenllkicvfifafimp
                                                                                                                                                                                                                                                                                             Human mu opiate receptor.
Mu opiate receptor; hMOR; opiate agonist; opiate antagonist;
drug abuse; analgesic.
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/note= "N-linked glycosylation site"
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30-JAN-1995; U01144.
28-JAN-1994; UG-188275.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
(USSH ) US SEC DEPT HEALTH.
(USSH ) US, Persico AM, Uhl G, Wang J;
NPI; 95-275422/36.
N-PSDB; Q93102.
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R76780 standard; Protein; 400
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                                                                                                                                                                                                                         Query Match 59.0%; Score 1675; DB 14; Length 400; Best Local Similarity 66.6%; Pred. No. 5.30e-142; Matches 207; Conservative 52; Mismatches 49; Indels 3; Gaps
hMOR cDNA was obtd. from a human cerebral cortical cDNA library screened with fragments of a rat mu opiate receptor. Expression of hMOR1 in COS cells revealed high affinity reconnition of the mu opiate specific ligand. Recombinant hMOR1 can be used to screen compounds for analgesic activity.
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm Thu Feb 17 11:14:24 2000; MasPar time 8.92 Seconds 552.170 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-455-683-2 (1-380) from USO8455683.pep 2839 1 MESPIQIFRGDPGPTCSPSA......RNTVQDPASMRDVGGMNKPV 380 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

131253 seqs, 12956647 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:Dackfiles1 Database:

Mean 32.927; Variance 157.770; scale 0.209 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Pred. No.	.11e-23	.11e-2	.39e-22	.75e-15	3e-13	.50e-13	.76e-13	.76e-13	.76e-1	.89e-12	,22e-12	.72e-12	.18e-12	8e-12	.04e-12	.52e-11	.94e-11	4e-11	.11e-11	.11e-11	le-11	e-11	e-10
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A,	-14	US-08-911-		US-08-454-	PCT-US94-1	US-08-454-	PCT-US94-1	-14	US-08-911-	US-08-454-	-41	US-08-411-	-91	-14	US-08-514-	US-08-514-		US-08-454-	-14	-55	-51	US-08-911-	-08-51
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1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	T US-08-149- XXXXXX	Sequence 7, Application US/0814  Sequence 7, Application US/0814  Patent No. 5558783  GENERAL INFORMATION:  APPLICANT: BURZOW, James R APPLICANT: Grandy, David K IITLE OF INVENTION: Opicid NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: ADDRESSEE: Banner & Alleg STREET: 10 South Wacker D CITY: Chicago STREET: 10 South Wacker D CITY: Chicago STREET: 11 nois CONTYER: BADABLE FORM: MEDIUM TYPE: Floppy disk CONTYTER: BATCHILD REPEASE CORPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: PatentIn Releas CORFUTER: PatentIn Releas CORFRAING SYSTEM: PC-DOS/ SOFTWARE: PatentIn Releas CURRENT APPLICATION NUMBER: US/08 FILING DAME: O6-NOV-1993 CLASSIFICATION: 438 ATTORNEY/AGENT INFORMATION: REFERNCE/DOCKET NUMBER: 35, TELEFAX: 312-715-1234 TELEFAX
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APPLICANT: Bulzow, James R
APPLICANT: Grandy, David K
TITLE OF INVENTION: A No. 5821067el Mammalian Methadone-Specific
TITLE OF INVENTION: Opioid Receptor Gene and Uses
                                                                                                                                                                                                                                                                                                                                            STSHSTAALSSYYPCIALGYTNSSLNPVLYAFLDENFKRCFRDFCFPIKMRMERQSTNRV 360
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                                                                                                                                                                                           Gaps
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                                         LOCATION: 1.380
OTHER INFORMATION: /label- identifier
OTHER INFORMATION: /note- "mouse Kappa-Opioid Receptor"
NCE 380 Aa, 42652 MW; 802929 CN;
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                                                                                                                                            Score 2826; DB 1; Length 380;
Pred. No. 3.11e-238;
0; Mismatches 2; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/911,245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
CITY: Chicago
COUNTRY: USA
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                                                                                                                                                 Query Match 99.5%;
Best Local Similarity 99.5%;
Matches 378; Conservative
                        NAME/KEY: Protein
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CLASSIFICATION:
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XX Sequence 7, Appli XX
C Sequence 7, Appli C SQLIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1..380
OTHER INFORMATION: /label= Identifier
OTHER INFORMATION: /note= "Mouse Kappa-Opioid Receptor"
VCE 380 AA; 42652 MW; 802929 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 2826; DB 2; I
Pred. No. 3.11e-238;
0; Mismatches 2;
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                    JMBER: US 08/149093
06-NOV-1993
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GENERAL INFORMATION:
APPLICANT: BUNZOW, James R. APPLICANT: Grandy, David K. APPLICANT: Grandy, David K. APPLICANT: Relnscheid, Rainer K. APPLICANT: Relnscheid, Rainer K.
                                                                                       NAME: NO. 5821067nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,311
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFRAX: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08514451A
                                                                                                                                                                                                             TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 7:
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                    APPLICATION NUMBER: US 0: FILING DATE: 06-NOV-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 RNTVQDPASMRDVGGMNKPV 380
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                 linear
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ADDALLS
STREET: 805 TILLS
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER REAGABLE FORM:
MEDUUR TYPE: Flopy disk
MEDUUR TYPE: Flopy disk
TYPE: POS/MS-DC
                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IISM: Rat
330 AA; 36851 MW; 611728 CN;
                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Darby & Darby, P.C.
STREET: 805 Third Avenue
CIIX: New York
                                                                                                                                   Sequence 5, Application US/08454549
Patent No. 5866324
                                                                                                          Sequence 5, Application US/08454549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                     STANDARD;
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Best Local Similarity 85.8%;
Matches 326; Conservative
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                                  US-08-454-549-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
APPLICANT: No. 5837809hacker, Hans-Peter APPLICANT: Monsma, Frederick J. TITLE OF INVENTION: A NOVEL MAMMALIAN OPIOID TITLE OF INVENTION: RECEPTOR LIGAND AND USES NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 2685; DB 2; I
Pred. No. 1.39e-225;
2; Mismatches 9;
                                                                                                                                                                         COMPUTER: IBM PC COMPATION COMPUTER: IBM PC COMPATION CASSIFICATION DATA:

PRICATION COMPATION COMPATION CASSIFICATION DATA:

PRICATION PAPLICATION DATA:

APPLICATION NUMBER: 08/55,058
FILING DAME: 11/13/95
FILING DAME: 11/13/95
FILING DAME: 11/13/95
FILING DAME: 08/55,058
FILING DAME: 08/55,058
FILING DAME: 08/55,058
FILING DAME: 08/55,058
FILING DAME: 08/378
TELEPRACION NUMBER: 899-4595/WDN
TELEPRACION INFORMATION: (503) 226-7391
TELEPRACION COMPATION: (503) 226-7391
TELEPRACION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                             ADDRESSEE: Klarquist Sparkman Campbell ADDRESSEE: Leigh & Whinston LLP STREET: 121 S.W. Salmon, Suite 1600 CITY: Portland STATE: Oregon
                                                                                                                                                                                                                                                                                                                                                       899-45995/WDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPTION: peptide
378 AA; 42392 MW; 806199 CN;
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amino acid
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Best Local Similarity 96.6%;
Matches 367; Conservative
                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy 1
                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                               Oregon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DESCRIPTION:
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                                                                                                                                                      97204
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                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 IITAVYSVVEVVGLVGNSLVMFVIIRYTKMKTATNIYIFNLALADALVTTIMPFQSAVYL 120
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                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: EPPLER, C. Mark
APPLICANT: OZENBERGER, Bradley A.
APPLICANT: HULMES, Jeffrey D.
TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
TITLE OF INVENTION: TO OPICID RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 MNSWPFGDVLCKIVISIDYYNMFTSIFTLTMMSVDRYIAVCHPVKALDFRTPLKAKIINI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPACTION SYSTEM: PC-DOS/MS-DUS
OPERATING SYSTEM: Patentin Release #1.0, Version #1.30
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Pred. No. 3.75e-154;
3; Mismatches 1;
330 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: RODINSON, JOSEPD R.
REGISTRATION NUMBER: 33,448
REPERENCE/POCKET NUMBER: 0446/1A818-US5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,549
FILING DATE: 30-MAX-1995
CLASSIFICATION: 435
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119 YLMNSWPFGDVLCKIVISIDYYNMFTSIFTLTMMSVDRYIAVCHPVKALDFRTPLKAKII 178
                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                        367 RIRQNTRDHPS 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM:
                                                                                                                                                                                                                         US-08-454-549-3
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Pred. No. 2.03e-135;
52; Mismatches 49; Indels 3; Gaps
                                                          STSHSTAVLSSYYFCIALGYTNSSLNPVLYAFLDENFKRCFRDFCFPIKMRMERQSTNRV
                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA

ZIP: 77210
COMPUTER RELABLE FORM:
MEDIOW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358
FILING DATE: Concurrently herewith
                                                                                                                                                                       400 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/120.601
FILING DATE: 13 SEPTEMBER 1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKEI NUMBER: INDA005P--
TELECHONE: (512) 418-300
TELEPHONE: (512) 418-300
                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Arnold, White & Durkee STREET: P. O. Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
JENCE 400 AA; 44779 MW; 873826 CN;
                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                       Sequence 8, Application PC/TUS9410358 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                     Sequence 8, Application PC/TUS9410358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    400 amino acids
                                                                                                                                                                       STANDARD;
                                                                                                      311 RNTVQDPASMRDVGGMNKPV 330
                                                                                                                     Query Match
Best Local Similarity 66.6%;
Matches 207; Conservative
                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1.
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                                                                                                                                                            RESULT 5
ID PCT-US94-10358-8
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247 VLIITVCYGLMILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVFIVCWTPIHIYVIIKA 306
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Patent No. 5866324
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OZENBERGER, C. Mark
APPLICANT: OZENBERGER, Bradley A.
APPLICANT: HOLMES, Jeffery D.
TITLE OF INVENTION: TO OPIOID RECEPTORS
UNMER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSED:
ADDRESS
NVCNWILSSAIGLPVMFMATTKYROG-S-IDCTLTFSHPTW-YWENLLKICVFIFAFIMP
                                                         Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSIEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NAME: US/08/454,549
FILING DATE: 30-MAY-1995
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ACASSIFICATION: 435
ACTORNEY/AGENT INFORMATION:
NAME: Robinson, Joseph R.
RECISTRATION INNERS: 33,448
REPERENCE/DOCKET NUMBER: 33,448
TREERENCE/DOCKET NUMBER: 0646/18918-US5
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08454549
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TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
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TOPOLOGY: linear
                        SEQUENCE
                                              Query Match
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                                                                               YLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDFRTPRNAKIV 187
                                                                                                                         68 AITIMALYSIVCVVGLFGNFLVMYVIVRYIKMKTAINIYIFNLALADALAISTLPFQSVN 127
             Gaps
                                                                                                            245 VLIITVCYGLMILRLKSVRMLSGSKEKDRNLRRITRMYLVVVAVFIVCWTPIHIYVIIKA
                                                                                                                                                               305 LITIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSTIEQQNST
             4;
           Indels
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COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
COMPUTER: IBM FOC COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
Pred. No. 2.50e-135;
53; Mismatches 50;
                                                                                                                                                                                                                                                                                                  398 AA.
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CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCI/US94/10358
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                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application PC/TUS9410358
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application PC/TUS9410358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/120.601
FILING DATE: 13 SEPTEMBER 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 37,259
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     398 amino acids
nino acid
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larity 66.1%;
Conservative
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FILING DATE: CONCUL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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Best Local Similarity
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TYPE: ar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILIITVCYGLMILRIKSVRMLSGSKEKDRNLRRITRMYLVVVAVFIVCWTPIHIYVIIKA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 LITIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSTIEQQNST 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A No. 5658783el Mammalian Methadone-Specific Opioid Receptor Gene and Uses
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 NYCNWILSSAIGLPVWEMATIKYRQG-S-IDCTLIFSHPTW-YWENLLKICVFIFAFIMP
                                                                                                                                                                       4;
                                                                                                            Length 398;
                                                                                                                                                                    Indels
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
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Patent No. 5658783
GENERAL INFORMATION:
APPLICANT: BUISCOW, James R
APPLICANT: Grandy, David K
TITLE OF INVENTION: A No. 5658783el Mammalian I
TITLE OF INVENTION: Oploid Receptor Gene and US
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
SIREE: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: 111inois
                                                                                                                                                              54; Mismatches 50;
                                                                                               Score 1674; DB 3;
Pred. No. 3.76e-135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                398 AA.
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FILING DATE: 06-NOV-1993
MOLECULE TYPE: protein
JENCE 398 AA; 44508 MW; 870781 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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ATIORNEY/AGENT INFORMATION:
NAME: No. 5658783nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08149093A
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TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIANDARD;
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                                                                                               Match Similarity 65.8%; Local Similarity 65.8%; les 208; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 365 RVRQNIREHPSTANTV 380
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SOFTWARE: Patenti
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SEQUENCE 5, APPLICA
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SEQUENCE 5, APPLICA
CC PATENT NO. 56878
CC APPLICANT: BUT
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CC APPLICANT: GA
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CC CLASSIFICATION PRINT
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US/08/911,245
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                                                                                                                            TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 5:
            FILING DATE: 15-AUG-1997
CLASSIFICATION: 536
                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 398 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   365 RVRQNTREHPSTANTV 380
                                                                                                                                                                                                                                                NAME/KEY: Protein
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359 RVR-NTVQDPASMRDV
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US-08-454-549-4
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Patent No. 5821067
GENERAL INFORMATION:
APPLICANT: Bunzow, James R
APPLICANT: Grandy, David K
TITLE OF INVENTION: A No. 5821067el Mammalian Methadone-Specific
TITLE OF INVENTION: A poid Receptor Gene and Uses
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                            299 LGSTSHSTAALSSYYFCIALGYTUSSLNPVLXAFLDENFKRCFRDFCFPIKMRMERQSIN 358
                                                                                                                                                                                                                68 AITIMALYSIVCVVGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVN 127
                                                                                                                                                                                                                                                            128 YLMGTWPFGTILCKIVISIDXYNMFTSIFTLCTMSVDRYIAVCHPVKALDFRIPRNAKIV 187
                                                                                                                                                                                                                                                                                                                                                                                                     LITIPETIFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPISSTIEQQNST 364
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                         245 ILIITVCYGLMILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVFIVCWTPIHIYVIIKA
                                                                                                                                                                                                                                                                                                           188 NVCNWILSSAIGLPVMFMATTKYRQG-S-IDCTLTFSHPTW-YWENLLKICVFIFAFIMP
                                                                                                                                                                                          4;
                                                                                                                                                                 Score 1674; DB 1; Length 398;
Pred. No. 3.76e-135;
54; Mismatches 50; Indels
                                                                                                                  R INFORMATION: /label= identifier
R INFORMATION: /note= "Rat Mu-Opioid Receptor"
398 AA; 44508 MW; 870781 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Banner & Allegretti, Ltd. STREET: 10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08911245
   TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 5:
                          SEQUENCE CHARACTERISTICS:
LENGTH: 398 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                     TOPOLOGY: linear MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                   ch 59.0%;
1 Similarity 65.8%;
208; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                NAME/KEY: Protein LOCATION: 1..398 OTHER INFORMATION: , OTHER INFORMATION: ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  359 RVR-NTVQDPASMRDV 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RVRQNTREHPSTANTV 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 10 South
CIIX: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-911-245-5
                                                                                                                                              SEQUENCE
                                                                                                                                                                   Query Match
                                                                                                                                                                                   Local
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68 AITIMALYSIVCVVGLFGNFLVMYVIVRYTKWKTATNIYIFNLALADALATSTLPFQSVN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 YLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRXIAVCHPVKALDFRTPRNAKIV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILIITVCYGLMILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVFIVCWTPIHIYVIIKA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 IGSTSHSTAALSSYYFCIALGYTNSSLNPVLYAFLDENFKRCFRDFCFPIKMRMERQSTN 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Patent No. 5866324
GENERAL INFORMATION:
APPLICANT: EPPLER, C. Mark
APPLICANT: OZENBERGER, Bradley A.
APPLICANT: HULMES, Jeffrey D.
TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
TITLE OF INVENTION: TO OPIOID RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NVCNWILSSAIGLPVMFMATTKYROG-S-IDCTLTFSHPTW-YWENLLKICVFIFAFIMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            339 VLIIVCYTLMILRIKKSVRLLSGSREKDRNLRRITKLVLVVVAVFIICWTPIHIFILVEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    305 LITIPETIFQIVSWHFCIALGYINSCLNPVLYAFLDENFKRCFREFCIPTSSTIEQQNST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 59.0%; Score 1674; DB 2; Length 39 Best Local Similarity 65.8%; Pred. No. 3.76e-135; Matches 208; Conservative 54; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1..398
OTHER INFORMATION: /label- Identifier
OTHER INFORMATION: /note= "Rat Mu-Opioid Receptor"
NCE 398 AA: 44508 MW; 870781 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367 AA.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149093
FILING DATE: 06-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5821067nan, Kevin E
REGISTRATION NUMBER: 35,313
FEBERENCE/DOCKET NUMBER: 93,311
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRI;
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GENERAL INFORMATION:
APPLICANT: BYANS, CHISTOPHER J.
APPLICANT: ENANS, CHISTOPHER J.
APPLICANT: EDNARDS, ROBERT H.
TITLE OF INVENTION: EXPRESSION CLONING OF A DELTA OPICID
TITLE OF INVENTION: RECEPTOR, RELATED EXPRESSION SYSTEMS, AND RELATED
TITLE OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: MOTISSON & POESTER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 ALAIAITALYSAVCAVGLLGNCLVMFGIVRYTKLKTAINIYIFNLALADALATSTLPFQS 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 AKYLMETWPFGELLCKAVLSIDYYNMFTSIFTLIMMSVDRYLAVCHPVKALDFRTPAKAK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 AIPVIITAVYSVVFVVGLVGNSLVMFVIIRYTKMKTATNIYIFNLALADALVTTTMPFQS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LINICIWVLASGVGVPIMVMAVTQPRDGA-VV-CMLQFPSP--SWYWDTVTRICVFLFAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVPILIITVCYGLMLLRLRSVRLLSGSKEKDRSLRRITRMVLVVVGAFVVCWAPIHIFVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                            SOFTWARE: PC-DOS/NS-DOS SOFTWARE: PC-DOS/NS-DOS CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/411,859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1598; DB 2; I
Pred. No. 2.22e-128;
51; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36,856
ER: 22000-20526.00
                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DAIA:
APPLICATION NUMBER: US 07/929,200
FILING DATE: 13-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
JENCE 372 AA; 40565 MW; 726402 CN;
                   Sequence 2, Application US/08411859 Patent No. 5985600
                                                                                                                                                                                                                                                 ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: LITHGOW, TIMOTHY J
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 56.3%;
Local Similarity 66.7%;
Nes 206; Conservative
                                                                                                                                                                                                           CITY: Palo Alto
STATE: California
COUNIRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 MFTSIFTLIMMSVDRYIAVCHFVKALDFRTPAKAKLINICIWVLASGVGVPIMVMAVTQP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 GSKEKDRSLRRITRMYLVVVGAFVVCWAPIHIFVIVWTLVDINRRDPLVVAALHLCIALG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLANVSDIFPSAFPSASANASGSPGAR--SAS-SLALAIAITALYSAVCAVGLLGNVLVM 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RDGA-VV-CTLQFPSP--SWYWDTVTKICVFLFAFVVPILLITVCYGLMLLRLRSVRLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 LLPNSSSWFPNWAESDSNGSVGSEDQQLESAHISPAIPVIITAVYSVVFVVGLVGNSLVW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/454,549 FILING DATE: 30-MAY-1995 CLASSTETAMENT.
                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Robinson, Joseph R.
REGIGSTRAILON NUMBER: 33,448
REFERENCE/DOCKET WUMBER: 0646/1A818-US5
TELECOMMUTICATION INFORMATION:
TELEFAX: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1610; DB 2; L
Pred. No. 1.89e-129;
55; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 AA; 40122 MW; 712609 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRI;
          CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, P.C.
STREET: 805 Third Avenue
CIIY: New York
                                                                                           ZIP: 100.2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YANSSLNPVLYAFLDENFKRCFRQLC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 YINSSLNPVLYAFLDENFKRCFRDFC 345
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                                                                                                                                                                                                                                                                                                                                                                                                                            SS: not relevant not relevant
                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 367 amino acids TYPE: amino acid STRANDEDNESS: not releva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 65.6%;
Matches 214; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
NUMBER OF SEQUENCES:
                                                                       New York
                                                                                                                                                                                                                   FILING DATE: 30 CLASSIFICATION:
                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
ORGANISM: Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: no MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
ID US-08-411-859-2
XX
AC XXXXXX
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DE Sequence 2, Applic
                                                                                    COUNTRY:
ZIP: 1002
                                                       CITY: N
STATE:
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TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7%;
Matches 206; Conservative
                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                  Illinois
                                                                                                                                                                                                                                                                           STREET: 10 sourtTY: Chicago
                                                                                                                                                                                                                                                                                                          USA
                                            343 GSLRRPRQA 351
                                                              355 QSTNRVRNT 363
                                                                                                                                                                                                                                                                                                        COUNTRY: US
                                                                                            T 13
US-08-911-245-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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                                                                                                                        XXXXXX
                                                                                          RESULT
ID US
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                                                                                                                                         TITLE OF INVENTION: EXPRESSION CLONING OF A DELTA OPTOID
TITLE OF INVENTION: RECEPTOR, RELATED EXPRESSION SYSTEMS, AND RELATED
TITLE OF INVENTION: PHARMACEUTICALS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORTISON & FOSISTER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 ALAIALTALYSAVCAVGLLGNVLVMFGLVRYIKLKTATNIYIFNLALADALATSTLPFQS 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 AKYLMETWPFGELLCKAVLSIDYYNMFTSIFTLTMMSVDRYIAVCHPVKALDFRTPAKAK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 VVPILIITVCYGLMLERLRSVRLLSGSKEKDRSLRRITRMVLVVVGAFVVCWAPIHIFVI 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LINICIWVLASGVGVPIMVMAVIQPRDGA-VV-CMLQFPSP--SWYWDTVTKICVFLFAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                               COUNTRY: USA

ZIP: 94304-1018
CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/411,859
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51; Mismatches 46;
        372 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1597; DB 2;
Pred. No. 2.72e-128;
                                                                                                                                                                                                                                                                                                                                                                                                  22000-20526.00
                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/929,200
FILING DATE: 13-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
CE 372 AA; 40561 MW; 727422 CN;
         PRT;
                                                                                                              APPLICANT: EVANS, CHRISTOPHER J. APPLICANT: KEITH JR., DUANE E. APPLICANT: EDWARDS, ROBERT H.
                                                                                  Sequence 10, Application US/08411859
Patent No. 5985600
GENERAL INFORMATION:
                                                                 Sequence 10, Application US/08411859
                                                                                                                                                                                                                                                                                                                                                                             NAME: LITHGOW, TIMOTHY J. REGISTRATION NUMBER: 36,856
                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 22
PELECONMUNICATION INFORMATION:
TELEPRONE: 415-813-5600
TELEFAX: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-494-0792
TELEEX: 706141
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    372 amino acids
         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206; Conservative
                                                                                                                                                                                                              CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
         US-08-411-859-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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12
                             XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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RESULT
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5,
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283 VWILVDINRRDPLVVAALHLCIALGYANSSLNPVLYAFLDENFKRCFRQLCRIPCGRQEP 342
                                                                                               Gaps
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LOCATION: 1.372
OTHER INFORMATION: /label= Identifier
OTHER INFORMATION: /note= "Mouse Delta-Opioid Receptor"
NCE 372 AA; 40617 MW; 728086 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/911,245
FILING DATE: 15-AUG-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1593; DB 2; L. Pred. No. 6.18e-128; 51; Mismatches 46;
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10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                  372 AA.
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FILING DATE: 1536
PRIOR APPLICATION DATE: 36
PRIOR APPLICATION DATE: 06-NOV-1993
FILING DATE: 06-NOV-1993
ATTORNEY AGENT INFORMATION:
NAME: No. 5811067nan, Revin E
REGISTRATION NUMBER: 35,303
REFERENCE/POCKET NUMBER: 93,311
TELEPHOME: 312-715-1000
TELEPHOME: 312-715-1134
                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08911245
Patent No. 5821067
GENERAL INFORMATION:
APPLICANT: Bunzow, James R
APPLICANT: Grandy, David K
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Patent No. 5658783
GENERAL INFORMATION:
APPLICANT: Burnow, James R
APPLICANT: Burnow, David K
TITLE OF INVENTION: A No. 5658783el Mammalian Methadone-Specific
TITLE OF INVENTION: Opioid Receptor Gene and Uses
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
                           ALAIAITALYSAVCAVGLIGNVLVMLGIVRYTKLKTAINIYIFNLALADALATSILPFQS 106
                                                                                                                                                                      LINICIWVLASGVGVPIMYMAVIQPR-DFAVV-CMLQFPSP--SWYWDTVIKICVFIFAF 222
                                                                                                                                                                                                                                                                                  AKYLMETWPFGELLCKAVLSIDYYNMFTSIFILTMMSVDRYIAVCHPVKALDFRTPAKAK
                                                                                                         VVPILIITVCYGLMLLRLRSVRLLSGSKEKDRSLRRITRMYLVVVGAFVVCWAPIHIFVI
                                                                                                                                                                                                                                                                                                                                             283 VWILVDINRRDPLVVAALHLCIALGYANSSLNPVLYAFIDENFKRCFRQLCRTPCGRQEP
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REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,311
TELECOMMUNICATION INFORMATION:
TELEFONE: 312-715-1000
TELEFAX: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08149093A
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amino acid
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STATE: Illinois
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US-08-149-093A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 LINICIWVLASGVGVPIMVMAVTQPR-DFAVV-CMLQFPSP--SWYWDIVTKICVFIFAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 VVPILIITVCYGLMLLRLRSVRLLSGSKEKDRSLRRITRMVLVVVGAFVVCWAPIHIFVI
NAME/KEY: Protein
LOCATION: 1..372
OTHER INPORMATION: /label= Identifier
OTHER INFORMATION: /note= "Mouse Delta-Opioid Receptor"
NCE 372 AA: 40617 MW; 728086 CN;
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9
                                                                                                                                                                                            Score 1593; DB 1; Length 372;
Pred. No. 6.18e-128;
51; Mismatches 46; Indels
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APPLICANT: Grandy, Dayld K.
APPLICANT: Civelli, Olivier
APPLICANT: Civelli, Olivier
APPLICANT: Reinscheid, Rainer K.
APPLICANT: No. 5837809hacker, Hans-Peter
APPLICANT: Monsma, Frederick J.
TITLE OF INVENTION: A NOVEL MAMMALIAN OPIOID
TITLE OF INVENTION: RECEPTOR LIGAND AND USES
NUMBER OF SEQUENCES: 16
CORRESSONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell
ADDRESSEE: Leigh & Whinston LLP
STREET: 121 S.W. Salmon, Suite 1600
CITY: Octinad
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/514,451A
FILING DATE: 08/11/95
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08514451A
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                                                                                                                                                                                                Query Match
Best Local Similarity 66.7%;
Matches 206; Conservative
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AC XXXXX

AX XXXXXX

DX XXXXXX

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CC Sequence 8, Applic

CC SETENT BUILDANT: BUILDAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 YIAVCHPVKALDFRIPRNAKIVNVCNWILSSAIGLPVNFMAITKYRQG-S-IDCTLTFSH 223
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Best Local Similarity 59.5%; Pred. No. 3.04e-126;
Matches 201; Conservative 60; Mismatches 73; Indels
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/553,058
FILING DATE: 11/13/95
ATTORNEY/AGENT: 11/13/95
ATTORNEY/AGENT: 11/13/95
ATGORNEY/AGENT: 11/13/95
REGISTRATION NUMBER: 30,878
REFERENCE/DOCKET NUMBER: 899-45995/WDN
TELECOMMUNICATION INFORMATION:
TELEFAN: (503) 228-9446
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 398 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: Amino acid
TYPE: AMINO acids
TYPE: A
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Search completed: Thu Feb 17 11:14:36 2000 Job time : 12 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Feb 17 11:12:22 2000; MasPar time 19.35 Seconds 786.860 Million cell updates/sec Tabular output not generated. Run on:

>US-08-455-683-2 (1-380) from USO8455683.pep 2839 1 MESPIQIFRGDPGFICSPSA.......RNIVQDPASWRDVGGMNKPV 380 Title: Description: Perfect Score:

Sequence:

PAM 150 Gap 11 Scoring table:

122810 segs, 40068593 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

1:pirl 2:pir2 3:pir3 4:pir4 pir60 Database:

Mean 49.052; Variance 117.295; scale 0.418 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARTES

		<b>%</b>			SUMMAKLES		
Result No.	Score	Query Match	Length	DB	Д	Description	Pred. No.
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2	2829	9	$\infty$	~	1	0.0000	00+000
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9	2610	Н	α	7	5525	kappa opioid recentor	
7	1687	9	7	C1	E008	delta opioid receptor	•
ω	1680	$\sigma$	6	N	S65693	Trecent	30-000
6	1678	$\sigma$	9	7	A57510	oid recentor	366-26
	1677	S	0	(7	I56553		100
11	1674	Q)	Φ,	N	156517	oid recept	910-016
12	1659	œ	Q	N	I56504		.07e-25
13	1612	Ø	7	C)	I38657	lta opia	-25
14	1610	o.	7	~	S34592	opioid	.36e-25
12	1608	Θ	7	C)	I38532	ta opicid	25-25
16	1597	9	1	C1	B48227	opioid	.66e-24
17	1473	m	9	N	I56520	20	836-22
18	1471	$\vdash$	9	~	JC2421	opioid receptor homel	116-22
19	1470	$\Box$	9	7	I49022		166-22
20	1465	$\vdash$	~	7	S43087	orphan opioid recepto	76-22
21	980	4	$\sigma$	7	C41795	somatostatin receptor	.26e-14
22	978	4	g	N	A39297		1e-14
23	976	34.4	σı	7	A41795		1.11e-139

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Gaps

Length 380; Indels

Score 2839; DB 2; L. Pred. No. 0.00e+00; 0; Mismatches 0;

Query Match Best Local Similarity 100.0%; Matches 380; Conservative

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33.9 38.2 JN0605 brain-specific semato 1.97e-133 38.6 38.4 2 JA7249 brain-specific semato 1.97e-133 38.6 38.4 2 JC4629 somatostatin receptor 7.06e-136 38.0 38.9 2 JC2083 somatostatin receptor 3.24e-131 38.1 369 2 JA1795 somatostatin receptor 7.36e-131 38.1 369 2 BA1795 somatostatin receptor 1.25e-128 38.2 33.2 188974 Somatostatin receptor 1.26e-132 38.8 36.4 2 INF955 somatostatin receptor 1.20e-112 28.8 36.2 2 INF955 somatostatin receptor 1.20e-112 28.8 36.4 2 INF955 somatostatin receptor 1.20e-112 27.9 36.8 2 INF974 Somatostatin receptor 1.20e-112 27.9 36.8 2 INF975 somatostatin receptor 1.20e-112 27.9 36.8 2 INF974 Somatostatin receptor 1.20e-112 27.9 36.8 2 INF974 Somatostatin receptor 1.20e-106 25.9 428 2 A44021 somatostatin receptor 1.20e-107 27.9 36.9 2 INF974 Somatostatin INF969 INF974 Somato	ALIGNMENTS  A48227 #type complete  kappa opioid receptor 1 - mouse  #formal_name Mus musculus #common_name house mouse 26-May-1994 #sequence_revision 26-May-1994 #text_change 10-Sep-1997  A48227: JC4138  A18227: JC4138  A18228: JC4138  A18228: JC4138  A18288: JC4138  A1	is receptor exists in different areas of the central and peripheral nervous systems, and mediates many physiological and pharmacological effects of opiates and opioid compounds.  kor  kor  brain; G protein-coupled receptor; glycoprotein; opioid peptide; phosphoprotein; transmembrane protein  #length 380 #molecular-weight 42652 #checksum 9937
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US-08-455-683-2.rpr

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Chen, Y.; Mestek, A.; Liu, J.; Yu, L.
Biochem. J. (1993) 295:625-628
Molecular cloning of a rat kappa opioid receptor reveals
sequence similarities to the mu and delta opioid receptors.
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Li, S.; Zhu, J.; Chen, C.; Chen, Y.W.; Deriel, J.K.; Ashby, B.; Liu-Chen, L.Y.
Bi-Liu-Chen, L.Y.
Bi-Chem. J. (1993) 295:629-633
Molecular cloning and expression of a rat kappa opioid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minami, M.; Toya, T.; Katao, Y.; Maekawa, K.; Nakamura, S. Onogi, T.; Kaneko, S.; Satoh, M. FEBS Lett. (1993) 329:291-295 Cloning and expression of a cDNA for the rat kappa-opioid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##cross-references GB:D16534; NID:g409390; PID:d1004487; PID:g415310
NCE
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                                                                                                                                                         IIIVCYTLMILRLKSVRLLSGSREKDRNLRRITKLVLVVVAVFIICWTPIHIFILVEALG 300
                                                                                                                                                                                                                        STSHSTAALSSYYFCIALGYTNSSLNPVLYAFLDENFKRCFRDFCFPIKMRMERQSTNRV 360
IITAVYSVVFVVGLVGNSLVMFVIIRYTKMKTATNIYIFNLALADALVTTTMPFQSAVYL 120
                                                                  MNSWPFGDVLCKIVISIDYYNMFTSIFTLTMMSVDRYIAVCHPVKALDFRTPLKAKIINI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                           kappa opioid receptor - rat
#formal_name Rattus norvegicus #common_name Norway rat
10-Dec-1993 #sequence_revision 19-Oct-1995 #text_change
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#cross-references MUID: 93380575 #accession S36143
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S36143; S38825; S36102; S39015; A48789
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Structure and chromosomal mapping of genes for the mouse
kappa-opioid receptor and an opioid receptor homologue
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#length 380 #molecular-weight 42630 #checksum 9705
                                                    #authors Meng, F.; Xie, G.
#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:9954-9958
#title cloning and pharmacological characterization of a :
#cross-references MUID:94052210
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##cross-references EMBL:000442; NID:9403486; PID:9403487

ADS G protein-coupled receptor; transmembrane protein

XI #length 380 #molecular-weight 42688 #checksum 99
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Pred. No. 0.00e+00;
3; Mismatches 1; Indels
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kappa opioid receptor - human
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Biochem. Biophys. Res. Commun. (1994) 202:1431-1437
Isolation of a human kappa opioid receptor cDNA from
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Score 2816; DB 2; Length 38
Pred. No. 0.00e+00;
0; Mismatches 2; Indels
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                                                            1 MESPIQIFRGEPGPTCAPSACLPPNSSAWFPGWAEPDSNGSAGSEDAQLEPAHISPAIPV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 IITAVYSVVFVVGLVGNSLVMFVIIRYTKMKTAINIYIFNLALADALVTTMPFQSTVYL 120
                                 Gaps
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                                                                                                                                                                                                                                              CIWLLSSSVGISAIVLGGTKVREDVDVIECSLQFPDDDYSWWDLFMKICVFIFAFVIPVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #gene GDB:OPRK1; KOR
##cross-references GDB:132651; OMIM:165196
#map_position 8q11.2-8q11.2
#MARY #length 380 #molecular-weight 42645 #checksum 8302
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Life Sci. (1995) 56:201-207
Cloning of a human .kappa. opioid receptor from
157005
 Score 2747; DB 2; Length 380; Pred. No. 0.00e+00;
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##cross-references GB:L37362; NID:g722617; PID:g722618
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#formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996
157005
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Pred. No. 0.00e+00;
18; Mismatches 6;
                              17; Mismatches
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larity 93.9%;
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Matches 356; Conservative
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##residues 1-38
               Similarity
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                                                                                                             ALGYINSSLNPILYAFLDENFKRCFRDFCFPIKMRMERQSTSRVRNTVQDPAYMRNVDGV 376
                                                       SISHSTAALSSYYFCIALGYTNSSLNPILYAFLDENFKRCFRDFCFPLKMRMERQSTSRV 360
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                                                                                                                                                                                                                                                                        #formal_name Cavia porcellus #common_name guinea pig
06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change
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                                          IIIVCYTLMILRIKSVRLLSGSREKDRNLRRITRLVLVVVAVFVVCWTPIHIFILVEALG
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 transmembrane protein
#length 380 #molecular-weight 42736 #checksum 7081
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##residues 1-380 ##label XIE
##cross-references GB:U04092; NID:g476105; PID:g476107
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kappa opioid receptor - guinea pig
dynorphin receptor
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Barrallo, A.; Gonzalez-Sarmiento, R.; Porterous, A.;
Garcia-Isidoro, M.; Rodriguez, R.E.
Garcia-Isidoro, M.; Rodriguez, R.E.
Blochem. Blophys. Res. Commun. (1998) 245:544-548
Cloning, molecular charaterization, and distribution of a gene homologous to delta opioid receptor from zebrafish (Danio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bare, L.A.; Mansson, E.; Yang, D. submitted to the EMPL Data Library, July 1994 submitted to two variants of the human mu opioid receptor mRNA in SK-N-SH cells and human brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 IAISITALYSVICVVGLLGNILVMYGVVRYTKLKTATNIYIFNLALADALATSTLPFQST 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 KYLMNTWPFGELLCKVVIAIDYYNMFTSIFTLTMMSVDRYIAVCHPVRALEFRIPIKAKI 170
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opioid receptor mu variant MORIA - human
#formal_name Homo sapiens #common_name man
12_Jul-1996 #sequence_revision 26-Jul-1996 #text_change
10-Sep-1997
                                                                                                                                                                                                                                                                                                                     ##residues 1-373 ##label BAR
##cross-references EXBL:ALO01596; NID:g2739230; PID:e1217996;
PID:g2739231
TT This protein mediates the effects of morphine and the related
drugs, and is the targets of endogenous opicid peptides.
DS glycoprotein
delta opioid receptor - Zebrafish
#formal_name Danio rerio
14-May-1998 #sequence_revision 29-May-1998 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 PVLVITICYGLMILRLKSVRLLSGSKEKDRNMRRITRMVLVVVAAFIICWTPIHIFIIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289 TLVDINQKNPFVIASWHLHRT-GYTNSSLNPVLYAFLDENFKRCFRDFCLPFRTRADQSN
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#length 373 #molecular-weight 42520 #checksum
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Pred. No. 3.50e-264;
62; Mismatches 42; Indels
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##residues 1-392 ##label BAR
##cross-references EMBL:U12569; NID:g607911;
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Similarity 65.6%;
206; Conservative
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mouse mu
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Magendzo, K.; Newman, D.; Tran, T.H.; Lee, D.S.; Wen, C.;
Xia, Y.R.; Lusis, A.J.; Evens, C.J.
J. Biol. Chem. (1995) 270:15877-15883
Characterization of the murine mu opioid receptor gene.
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##cross-references GB:U19380
NNCE Min, B.H.; Augustin, L.B.; Felsheim, R.F.; Fuchs, J.A.; Loh,
Ithors Min, B.H.; Augustin, L.B.; Felsheim, R.F.; Fuchs, J.A.; Loh,
 variants of the human mu opioid receptor cells and human brain.
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#formal_name Mus musculus #common_name house mouse
08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change
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Antisense mapping the MOR-1 opioid receptor: evidence alternative splicing and a novel morphine-6 beta-glucuronide receptor.
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promoter sequence of a
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                                                                                   387-392 ##label BAW
#length 392 #molecular-weight 43939 #checksum
                                                                                                                                         Length 392;
                                                                                                                                    Score 1680; DB 2; Length 39
Pred. No. 6.02e-263;
53; Mismatches 56; Indels
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Genomic structure analysis of
opioid receptor gene.
ness MUID:94377496
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#title Expression of two mRNA in SK-N-SH #Cross-references MUID:95046336 #accession S51216
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L Similarity 65.0%;
210; Conservative
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##residues 1-39
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#journal J. Neurosci. (1995) 15:2396-2406

#title Ihe human mu opioid receptor: modulation of functional desensitization by calcium/calmodulin-dependent protein kinase and protein kinase C.

#accession 156553
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Opiate receptor mu - human
MOR1 protein; opioid receptor mu
#formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
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alternative splicing; G protein-coupled receptor;
glycoprotein; transmembrane protein
#length 398 #molecular-weight 44421 #checksum 8164
                                                               ##residues 17 1398 ##label ROS ##cross-references EMBL:026915; NID:91055230; PID:91055231 ##note the nucleotide sequence was submitted to the Library, November 1995
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                                  nucleic acid sequence not shown; translation
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##cross-references GB:L29301; NID:9459831
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Griffin, C.A.; Uhl, G.R.
submitted to GenBank, August 1994
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tcross-references MUID:95377399
taccession 866513
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##residues 1-398
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                                                                                                                      Human mu opiate receptor. cDNA and genomic clones, pharmacologic characterization and chromosomal assignment
                                                                                                                                                                                                                                                             #authors Bare, L.A.; Mansson, E.; Yang, D.
#journal FEBS Lett. (1994) 354:213-216
#title Expression of two variants of the human mu opioid receptor mRNA in SK-N-SH cells and human brain.
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Wang, J.B.; Johnson, P.S.; Persico, A.M.; Hawkins, A.L.; Griffin, C.A.; Uhl, G.R. FEBS Lett. (1994) 338:217-222
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#map_position 6q24-6q25
KEYWORDS G protein-coupled receptor; glycoprotein; transmembrane protein
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##residues 1-50,'N',52-233,'V',235-400 ##label WAN ##cross-references GB:L25119; NID:g452072; PID:g452073
                                                                                                                                                                                                    nucleic acid sequence not shown
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##residues 1-50,'N',52-400 ##label WA2
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##rnosidnes 387-400 ##label BAR
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mu opioid
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Fukuda Fukuda K.; Kato, S.; Mori, K.; Nishi, M.; Takeshima, H.
#Journal FEBS Lett. (1993) 327:311-314
#title Primary structures and expression from CDNAs of rat opioid
#cross-references WUID:93351652
                                                                                                                                                                                                                                                                                                                                                               #authors Chen, Y.; Mestek, A.; Liu, J.; Hurley, J.A.; Yu, L.
#journal Mol. Pharmacol. (1993) 44:8-12
#title Molecular cloning and functional expression of a mu-opio.id
receptor from rat brain.
#cross-references MUID:93341493
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#journal Biochem. Biophys. Res. Commun. (1995) 209:563-574
#title Complementary DNA cloning of a mu-opioid receptor from rat peritoneal macrophages.
#cross-references MUID:95251654
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#formal_name Rattus norvegicus #common_name Norway rat
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
29-Jan-1999
156517; 157951; A49680; I52314; S34593; A48799; I58154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors Eppler, C.M.; Hulmes, J.D.; Wang, J.B.; Johnson, M.; Luthin, D.R.; Uhl, G.R.; Linden, J. #journal J. Biol. Chem. (1993) 268:2647-26451 #title Purification and partial amino acid sequence of a receptor from rat brain.
                                                                                                                                                                                                                                      ##status preliminary; translated from GB/EMBL/DDBJ#mare.a.type mRNA ##race.a.type mRNA
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##residues 1-244,'V',246-398 ##label WAN
##rcss-references GB:L20684; NID:g409149; PID:g409150
SNCE 158154
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O.K.; Kelly, M.J.; Grandy, D.K.
J. Neurochem. (1995) 64:14-24
Characterization and distribution
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##residues 272-291 ##label EPP
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J.; Briones-Urbina, R.; O'Dowd, B.F.
J. Neurochem. (1994) 62:2099-2105
Cloning, characterization, and distribution of a mu-opioid
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#formal_name Rattus norvegicus #common_name Norway rat
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
26-Jul-1996
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Thompson, R.C.; Mansour, A.; Akil, H.; Watson, S.J. Neuron (1993) 11:903-913
Cloning and pharmacological characterization of a rat
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G protein-coupled receptor; transmembrane protein
#length 398 #molecular-weight 44508 #checksum 8374
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Pred. No. 6.91e-262;
54; Mismatches 50; Indels
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Pred. No. 3.07e-259;
53; Mismatches 51; Indels
                                                                                                                                          ##residues 1-244,'V',246-398 ##label THO ##cross-references GB:L22455; NID:g437671; PID:g437672
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##residues 1-398 ##label RES
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#cross-references MUID:94059560 Faccession I58154
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Best Local Similarity 65.8%;
Matches 208; Conservative
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Simonin, F.; Befort, K.; Gaveriaux-Ruff, C.; Matthes, H.; Nappey, V.; Lannes, B.; Micheletti, G.; Kieffer, B. Mol. Pharmacol. (1994) 46:1015-1021
The human delta-opioid receptor: genomic organization, cDNA cloning, functional expression, and distribution in human brain.
                    YLMGTWPFGTILCKIVISIDYYNMFTSIFILCTMSVDRYIAVCHPVKALDFRTPRNAKIV 187
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delta opiate receptor - human
#formal_name Homo sapiens #common_name man
06.Sep-1996 *sequence_revision 06-Sep-1996 #text_change
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M.; Santoro, G.; Varga, E.V.; Hruby, V.J.; Roeske, W.R.;
Yamanuza, H.I.
Life Sci. (1994) 54:PL463-PL469
Identification of a human delta opioid receptor: Cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                      #authors Fukuda, K.; Kato, S.; Mori, K.; Nishi, M.; Takeshima, H. FEBS Lett. (1993) 327:311-314
#title Primary structures and expression from cDNAs of rat opioid #cross-references MUID:93351652
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                                                                                                                                                                                                                                                                                                      ##residues 1-372 ##label FUK ##cross-references GB:D16348; NID:g391864; PID:d1004367; PID:g391865
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#type complete
delta opioid receptor - rat
#formal_name Rattus norvegicus #common_name Norway rat
10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change
29-Jan-1999
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delta opioid receptor - human
#formal_name Homo sapiens #common_name man
29-May-1998 #sequence_revision 29-May-1998 #text_change
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J. Neurosci. Res. (1994) 27:714-719
Molecular cloning and expression of a rat delta opioid
receptor from rat brain.
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#length 372 #molecular-weight 40449 #checksum 2221
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Pred. No. 1.36e-250;
55; Mismatches 48; Indels
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О
                                                                                                                                                                               Length 372;
                                                        preliminary; translated from GB/EMBL/DDBJ
                                                                                             ##residues 1-372 ##label RES ##coss-references EMBL:U07882; NID:g497313; PID:g497314 ##cross-references EMBL:U07882; NID:g497313; PID:g497314 #coss-references EMBL:U07882; NID:g497313; PID:g497314 #checks:
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Pred. No. 3.06e-250;
56; Mismatches 48;
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               *cross-references MUID:94260835
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ilarity 65.3%;
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expression
                                                                              ##molecule_type mRNA
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

MasPar time 13.32 Seconds 806.224 Million cell updates/sec Thu Feb 17 11:13:01 2000; Run on:

Tabular output not generated.

Title:

>US-08-455-683-2 (1-380) from USO8455683.pep 2839 1 MESPIQIFRGDPGPTCSPSA......RNTVQDPASMRDVGGMNKPV 380 Description: Perfect Score: Sequence:

Scoring table:

77977 segs, 28268293 residues PAM 150 Gap 11 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot37 1:swissprot

Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 50.173; Variance 102.089; scale 0.491

Statistics:

## SUMMARIES

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## ALIGNMENTS

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                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no nay modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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TISSUE SPECIFICITY: BRAIN (NEOCORIEX, HIPPOCAMPUS, AMYGDALA, MEDIAL HABENULA, HYPOTHALAMUS, LOCUS CERULEUS, AND PARABRACHIAL
                                      SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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PFAM; PF00001; 7fm_1; 1.
G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
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Pred. No. 0.00e+00;
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                                                                                                                                                                                      , D31663; G808876; JOINED.

, D31664; G808876; JOINED.

, S77872; G998532; -.

, S77868; G998532; JOINED.

, S77869; G998532; JOINED.

, S81111; E257489; -.
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Similarity 100.0%;
80; Conservative
                                                                                                                                                                EMBL; L11065; G348249; -. EMBL; D31665; G808876; -.
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PIR; A48227; A48227
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380 AA;
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"Cloning and expression of a CDNA for the rat kappa-opioid receptor."; FEBS LETT. 329:291-295(1993).
                                                                                       IIIVCYTLMILRLKSVRLLSGSREKDRNLRRITKLVLVVVAVFIICWTPIHIFILVEALG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NISHI M., TAKESHIMA H., FUKUDA K., KATO S., MORI K.; "CDNA cloning and pharmacological characterization of an opioid receptor with high affinities for kappa-subtype-selective ligands."; FEBS LETT. 330:77-80(1993).
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YAKOVLEV A.G., KRUEGER K.E., FADEN A.I.;
"Structure and expression of a rat kappa opioid receptor gene.";
J. BIOL. CHEM. 270:6421-6424(1995).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHEN Y., MESTER A., LIU J., YU L.;
Molecular cloning of a rat kappa opioid receptor reveals sequence
similarities to the mu and delta opioid receptors.";
BIOCHEM. J. 295:625-628(1993).
                   241 IIIVCYTLMILREKSVRLESGSREKDRNLRRITKLVLVVVAVFIICWTPIHIFILVEALG
                                                                   STSHSTAALSSYYFCIALGYTNSSLNPVLYAFLDENFKRCFRDFCFPIKMRMERQSTNRV
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RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
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MEDILIE; 93374033.
WINAMI M. TOYA T., KATAO Y., MAEKAWA K., NAKAMURA S., ONOGI
KANEKO S., SATOH M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 9405210.
MENG F., XTE G.-X., THOMPSON R.C., MANSOUR A., GOLDSTEIN A., MATSON S.J., AKIL H.;
"Cloning and pharmacological characterization of a rat kappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZHU J., CHEN C., CHEN Y.-W., DERIEL J.K., ASHBY B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90:9954-9958(1993).
                                                                                                                                                                                                                        2 STANDARD; PRT; 380 AA. 0PRK, 24975, 11-FEB-1994 (REL. 28, CREATED) 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE) 01-NOT-1997 (REL. 35, LAST ANNOTATION UPDATE) OPRKI OR ROR-D.
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STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
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STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
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                                                                                                                                       RNTVQDPASMRDVGGMNKPV 380
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STRAIN-WISTAR; TISSUE-BRAIN;
MEDLINE; 93380575.
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MEDLINE; 94059008.
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LIU-CHEN L.-Y
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GCRDB; GCR_1819; -. GCRDB; GCR_2026; -. GCRDB; GCR_2054; -.
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MEDLINE; 94338360.
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SEQUENCE FROM N.A.
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MEDLINE; 95350200.
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OPRK_HUMAN
P41145;
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                                                                                                 This SWISS-PROI entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF AUTONOMIC AND NEUROBDOCRINE FUNCTIONS. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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5 (POTENTIAL).
5 (YOTENTIAL).
6 (POTENTIAL).
6 (POTENTIAL).
EXIRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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PROSITE; PSOGGO1, 7-
PRAM; PPOODO1, 7-
PRAM; PPOODO1, 7-
G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
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3 (POTENTIAL).
CXTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
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C -> Y (IN REF. 3).
EE858A46 CRC32;
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98.98;
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nes 376; Conser
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GCR_0790;
GCR_0804;
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Matches
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ZHU J., CHEN C., XUE J.-C., KUNAPULI S., DERIEL J.K., LIU-CHEN L.-Y.

"Cloning of a human kappa opioid receptor from the brain.";

LIFE SCI. 56:201-207(1995).

-1- FUNCTION: INHIBITS NEUFORTRANSMITTER RELEASE BY REDUCING CALCIUM
ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                         STSHSTAALSSYYFCIALGYINSSLNPVLYAFLDENFKRCFRDFCFPIKMRERQSTNRV
CIWLLASSVGISAIVLGGTKVREDVDVIBCSLQFPDDEYSWWDLFMKICVFVFAFVIPVL
                                          IIIVCYTLMILRLKSVRLLSGSREKDRNLRRITKLVLVVVAVFIICWTPIHIFILVEALG
                                                                      IIIVCYTLMILRIKSVRLLSGSREKDRNIRRITKIVLVVVAVFIICWTPIHFILVEALG
                                                                                                                       STSHSIAVLSSYYFCIALGYINSSLNPVLYAFLDENFKRCFRDFCFPIKMRMERQSTNRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MANSSON E., BARE L.A., YANG D.; "Isolation of a human kappa opioid receptor cDNA from placenta."; BIOCHEM. BIOPHYS. RES. COMMUN. 202:1431-1437(1994).
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SIMONIN F., GAPTERIAUS-RUFF C., BEFORT K., LANNES B., MICHELETTI (
MATTEL M.-G., CHARON G., BLOCH B., KIEFFER B.;
"Kappa-Cpicid receptor in humans: cDNA and genomic cloning,
chromosomal assignment, functional expression, pharmacology, and
expression pattern in the central nervous system.";
PROC. NATL. ACAD. SCI. U.S.A. 92:7006-7010(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOMO SAPIENS (HUMAN).
EURARYOTA: MEJAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
12-UL-1998 (REL. 36, LAST ANNOTATION UPDATE)
RAPPA-TYPE OPICID RECEPTOR (KOR-1).
                                                                                                                                                                                                                                                                                                                               380 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIMATES; CATARRHINI; HOMINIDAE; HOMO
                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                              380
                                                                                                                                                                                                        RNTVQDPASMRDVGGMNKPV 380
                                                                                                                                                                                                                             RNTVQDPASMRDVGGMNKPV
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                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCRDB; GCR_2054;
MIM; 165196; -.
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                                                                                                                                                                                                                                                                                                     Length 380;
                                                        1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
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PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1. PFAM; PF00001; 7tm_1; 1. G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
                                                                                                                                                                                    EXTRACELLULAŘ (POTENTIAL).
7 (POTENTIAL).
                                   PALMITATE.
EXTRACELLULAR (POTENTIAL).
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1980629E CRC32;
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CYTOPLASMIC (POTENTIAL).
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
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Pred. No. 0.00e+00;
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ANNOTATION UPDATE)
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17; Mismatches
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01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQI
01-NOV-1997 (REL. 35, LAST ANN
KAPPA-TYPE OPIOID RECEPTOR (KOI
                                                                                                                                                                                                                                                                                MM;
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SEQUENCE FROM N.A.
STRAIN-HARTLEY; TISSUE-BRAIN;
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                                   PHOSPHORYLATION; LIPOPROTEIN;
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93.9%;
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222
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nes 357; Conser
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     MILE G. X., MENG F., MANSOUR A., THOMPSON R.C., HOVERSTEN M.T., GOLDSTEIN A., WAILE B., PERGEREN S.J., AKIL H.;
GOLDSTEIN A., WAISON S.J., AKIL H.;
PERGEN STRUCTURE and functional expression of a guinea pig kappa opioid (dynorphin) receptor., PROC. NATL. ACAD. SCI. U.S.A. 91:3779-3783(1994).

-I- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM ION CURRENTS AND INCREASING POPASSIUM ION CONDUCTANCE. RECEPTOR FOR DYNORPHINS. ANY PLAY A ROLE IN AROUSAL AND REGULATION OF AUTONOMIC AND NEUROBNOCKINE FUNCTIONS.

-I- SUBCELLULAR LOCATION: INTEGRAL MEMBERANDE PROTEIN.

-I- SIMILARITY: BELONGS IO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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PFAM; PF00001; 7tm_l, 1.
G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLXCOPROTEIN; PHOSPHORYLAFION; LIPOPROTEIN; PALMITATE.
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Pred. No. 0.00e+00;
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CYTOPLASMIC (P
4 (POTENTIAL).
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CYTOPLASMIC (1
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92.9%;
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39
380 AA;
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Best Local Similarity
Matches 338; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-LIVER;
MEDLINE; 94377496.
MIN B.H., AUGUSTIN L.B., FELSHEIM R.F., FUCHS J.A., LOH H.H.;
"Genomic structure analysis of promoter sequence of a mouse mu opioid receptor gene.";
PROC. NATL. ACAD. SCI. U.S.A. 91:9081-9085(1994).
"Characterization of the murine mu opioid receptor gene.";
J. BIOL. CHEM. 270:15877-15883(1995).
-!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR FOR BETA-ENDORPHIN.
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE, 95377399.
ROSSI G.C., PAN Y.X., BROWN G.P., PASTERNAK G.W.; "Antisense mapping the MOR-1 opioid receptor: evidence for alternative splicing and a novel morphine-6 beta-glucuronide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BALB/C; TISSUE-BRAIN;
MEDLINE; 93318184.
KAUTRAN D.L., FEITH D.E., ANTON B., TIAN J., MAGENDZO K.,
MEWAAN D., IRAN T., LEE D.S., WEN C., XIA Y., LUSIS A.J.,
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G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
                                                                                                                                                                                                                    P42866; Q60768;
01-NOY-1995 (REL. 32, CREATED)
01-NOY-1995 (REL. 32, LAST SEQUENCE UPDATE)
FJUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
MU-TYPE OPICID RECEPTOR (MOR-1).
                                                                                                                                                                                                      398 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:9741; OPRM.
PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
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                                                                                                                                                                                                      PRT;
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EMBL, U10558, G565069; JOINED.
EMBL, U10559; G565069; JOINED.
EMBL, U10560; G565069; JOINED.
EMBL, U10560; G865069; JOINED.
EMBL, U19380; G885865; -.
GCRDB; GCR.1312;
GCRDB; GCR.1699; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEBS LETT. 369:192-196(1995)
                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                     OPRMI OR OPRM OR MOR. MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                               377 NKPV 380
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OPRM_MOUSE
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MEDLINE; 94139928.
WANG J.-B., JOHNSON P.S., PERSICO A.M., HAWKINS A.L., GRIFFIN C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Human mu opiate receptor. cDNA and genomic clones, pharmacologic characterization and chromosomal assignment.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
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PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1678; DB 1; Length 398;
Pred. No. 0.00e+00;
55; Mismatches 49; Indels
                                                                                                                                     Z (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

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C0211489 CRC32;
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OPRM HUMAN
STANDARD; PRT; 400 AA.
035372, 012930;
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
MU-TYPE OPICID RECEPTOR (MOR-1).
                                                        (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 59.18; Local Similarity 65.88;
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                                                                                                                                                            IISSUE-BRAIN,
MEDLINE; 95046336.
BARE LA., MANSSON E., YANG D.;
MEDLINE; 95046336.

EARPESSION Of two variants of the human mu opioid receptor mENA in SK-N-SH cells and human brain.";
FEBS LETT. 354:213-216(1994).

-! FUNCTION: INHIBITS NUMCOTRANSMITTER RELEASE BY REDUCING CALCIUM ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR FOR BETA ENDORPHIN.

-! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-! SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

-! SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSIES, PS00237; G_PROTEIN_RECEPTOR; 1.

PFAM: PF00001; 7tm_1: 1.

G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;

PHOSPHORYLATION: LFOPPOTEIN: PALMITATE: ALTERNATIVE SPLICING.

DOMAIN 1 66 EXTRACELLULAR (FOTENIIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> VRS (IN MOR1A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1677; DB 1; Length 400; Pred. No. 0.00e+00;
                                                            MESTEK A. JR., HURLEY J.H., BYE L.S., CAMPBELL A., TIAN M., CHEN Y., YU L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLUIAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
PALMITATE (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                    SUBMITTED (XXX-1994) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N -> D (IN REF. 3).
D -> N (IN REF. 1).
M -> I (IN REF. 3).
L -> V (IN REF. 1).
7; IAFCO337 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 (POTENTIAL).
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Local Similarity 66.6%;
les 207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L25119; G452073; -.
EMBL; L29301; G459832; -.
EMBL; U12569; G607912; -.
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207
234
400 AA;
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                                                                                                                                                 SEQUENCE FROM N.A.
[2]
SEQUENCE FROM N.A.
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                                            IISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
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49; Indels

52; Mismatches

Matches

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70 AITIMALYSIVCVVGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVN 129

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PVIITAVYSVVEVVGLVGNSLVMFVIIRYTKMKTATNIYIFNLALADALVTTTMPFQSAV 118
                                                                                                         246
                                                                                                                                                                                                                                             THEN Y., MESTER A., LIU J., HURLEY J.A., YU L.; Molecular cloning and functional expression of a mu-opioid receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUKUDA K., KATO S., MORI K., NISHI M., TAKESHIMA H.; "Primary structures and expression from cDNAs of rat opioid receptor
                                                              VLIITVCYGLMILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVFIVCWTPIHIYVIIKA
                                                                                                                                                                                                                             LVTIPETTEQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSNIEQQNST
                                            YLMGIWPFGTILCKIVISIDYYNNFTSIFTLCTMSVDRYIAVCHPVKALDFRIPRNAKII
                                                                                                       NVCNWILSSAIGLPVMFMATTKYRQG-S-IDCTLTFSHPTW-YWENLLKICVFIFAFIMP
                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-SPRACUE-DAWLEY; TISSUE-OLFACTORY BULB;
MEDLINE; 9405956.
THOMPSON R.C., MANSOUR A., AKIL H., WATSON S.J.;
"Cloning and pharmacological characterization of a rat mu opioid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WANG J.-B., IMAI Y., EPLER M.C., GREGOR P., SPIVAK C., UHL G.R., "Mu opiate receptor: cDNA cloning and expression.", PROC. NAIL. ACAD. SCI. U.S.A. 90:10230-10234(1993).
EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                     P33535; Q64064; Q624120; C1-FEB-1994 (REL. 28, CREATED) (01-FEB-1994 (REL. 28, CREATED) (01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE) (15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) (MU-TYPE CAPPIOL RECEPTOR (MOR-1) (OPIOID RECEPTOR B) (MUORI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BUNZOW J.R., GRANDY D.K., KELLY M.;
SUBMITIED (SEP-1993) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                   398 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHARMACOL. 44:8-12(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 delta- and mu-subtypes.";
FEBS LETT. 327:311-314(1993).
                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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MEDLINE; 93351652.
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MEDLINE; 93341493.
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SEQUENCE FROM N.A.
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                                                 "Cloning, characterization, and distribution of a mu-opioid receptor
                                                                                                                                                                                                                                                               FEBS LETT. 359:142-146(1995).
                                                                                                                                                                                                   SEQUENCE OF 356-391 FROM N.A.
MEDDINE; 95172221.
ZIMPRICH A., SIMON T., HOLLT V.;
"Cloning and expression of an isoform of the rat mu opioid receptor (rMORIB) which differs in agonist induced desensitization from
                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: BRAIN. IS EXPRESSED IN THE CEREBRAL CORTEX,
CAUDATE PUTAMEN, NUCLEDA ACCUMENS, SEPTAL NUCLEI, THALAMUS,
HIPPOCAMPUS, AND HEBSULIA. NOT DETECTED IN CEREBELLUM.
SIMILARITY: BELONGS IO FAMILY 1 OF G-PROTEIN COUPLED RECEPIORS.
                         NGUYEN T., CHENG R., TSATSOS J.,
                                                                                                                                      SEDQI M., ROY S., RAMAKRISHNAN S., ELDE R., LOH H.H.;
Complementary DNA cloning of a mu-opioid receptor from rat
peritoneal macrophages.";
BIOCHEM. BIOPHYS. RES. COMMUN. 209:563-574(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCRDB, GC. 22561; -
PROSIDE; PSC0237; G_PROTEIN_RECEPTOR; 1.
PFAM; PF0001; 7tm_1; 1
G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; PHOSPHORYLAIION; LIPOPROTEIN; PALMITATE.
PHOSPHORYLAIION; LIPOPROTEIN; PALMITATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
SYTRACELLUGAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELUTAR (POTENTIAL)
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
                                                           in rat brain.";
J. NEUROCHEM. 62:2099-2105(1994).
          MEDLINE; 94246380.
ZASTAWNY R.L., GEORGE S.R., NG
BRIONES-URBINA R., O'DOWD B.F.
                                                                                                 SEQUENCE OF 101-340 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, 113069, G348251, -
EMBL, U020683, G407574, -
EMBL, U22455, G407672, -
EMBL, U35424, G1017732, -
EMBL, S778683, E199500, -
EMBL, S75669, G861432, -
PIR, S34593; S34593.
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GCR_0637;
GCR_0640;
GCR_0640;
GCR_1001;
GCR_1101;
                                                                                                              TISSUE=MACROPHAGE;
MEDLINE; 95251654.
IISSUE-BRAIN;
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GCRDB;
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                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                             119 YLMNSWPFGDVLCKIVISIDYYNMFTSIFTLIMMSVDRYIAVCHPVKALDFRTPLKAKII 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLIITVCYGLMILRLKSVRMLSGSKEKDRNLRRIFRWYLVVVAVFIVCWTFIHIYVIIKA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 AITIMALYSIVCVVGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVN 127
                                                                                                                                                                                                                                                                                                                                                                                                              YLMGTWPFGIILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDFRIPRNAKIV 187
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAMPUSCH M.P., OSINSKI M.A., BROWN D.R., MURTAUGH M.P., SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.

-!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDCING CALCIUM IN CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR FOR BETA-ENDORPHIN.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NICIWLLASSVGISAIVLGGIKVREDVDVIECSLQFPDDEYSWWDLFMKICVFVFAFVIP
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                                                                                                                                                                                                                                                                    Score 1676; DB 1; Length 398; Pred. No. 0.00e+00;
                                                                                                     POIENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
F - S (IN REF. 6).
V -> I (IN REF. 3, 4 AND 7).
LENLE -> KTYLE (IN REF. 8).
                                                                                                                                                                                                                                                                                                         Indels
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
PALMITARE (POTENTIAL).
POTENTIAL.
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01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                         53; Mismatches
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66.1%;
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   SEQUENCE FROM N.A.
TISSUE=BRAIN CORTEX;
                                                                                                                                                                                                                                                                                     Best Local Similarity
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387
398 AA;
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EMBL; U89677; G1881731; -
                                       FOR BETA-ENDORPHIN
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401
354
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RVRNTVQDPAS 369
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Matches 205; Conser
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TISSUE-STRIATUM;
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                                                                                                                                                                                                                                                                                                              YLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDFRTPRNAKII 190
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                                                                                                                                                                                                                                                                Gaps
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACTYLA; RUMINANTIA; PECORA; BOYOIDEA; BOVIDAE; BOYINAE; BOS.
                                                                                                                                                                                                                                                                                                                       NVCNWILSSAIGLPVMFMATTKYRNG-S-IDCALTFSHPTW-YWENLLKICVFIFAFIMP
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                                                                                                                                                                                                                                                                ë
                                                                                                                                                                                                                                              Score 1672; DB 1; Length 401;
Pred. No. 0.00e+00;
52; Mismatches 49; Indels
                PROSTIE; PS00237; G PROTEIN_RECEPTOR; 1.
PFAM; PF00001; 7tm_1; 1.
G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
DOMAIN 1 67 EXTRACRITATION COMPANY.
                                                             1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                    6 (POTENTIAL).
EXTRACELIDIAR (POTENTIAL).
7 (POTENTIAL).
                                                                                                                    EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                  PALMITATE (POTENTIAL)
                                                                                                                                                                                                                               6786FD94 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPRM_BOVIN STANDARD; PRT; 401 AA. P79350; 15-JUL-1998 (REL. 36, CREATED) 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                         7 (POTENTIAL)
                                                                                                                                                                           BY SIMILARITY
                                                                                                            4 (POTENTIAL)
       EMBL; L38645; G1553057; -.
GCRDB; GCR_1287; -.
PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
                                                                                                                                                                                                  POTENTIAL.
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                                                                                                                                                                                                                               401 AA;
                                                                                                                                                                                                                                                        Local Similarity
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SEQUENCE FROM N.A.
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                                                             TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247
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SIMON E.J., VILLEM S., ANDRIA M., ONORISHVILI I., HILLER J.M.; SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: INHIBITS NEDROTRANSHITTER RELEASE BY REDGING CALCIUM ION CURRENIS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
                                                                                                                          -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 ILIITYCYGLMILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVFIVCWTPIHIYVIIKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308 LITIPETIFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSTIEQQNST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 YLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDLRTPRNAKII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 401;
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                                                                                                                                                                                                                                                                                                                                                                                                                             GCRDB, GCR_1213; -...
PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
PFAM; PF00001; 7tm_1; 1.
G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 (POTENTIAL).
EXTRACELLOLAR (POTENTIAL).
7 (POTENTIAL).
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1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
PALMITATE (POTENTIAL).
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54; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1650; DB 1; 1
Pred. No. 1.71e-302;
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5673B9B8 CRC32;
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.larity 65.9%;
.Conservative
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POTENTIAL.
18
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41
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348
370
40368 MW; 4
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FEBS LETT. 327:311-314(1993)
                                                                                                        similarity 63.1%;
                                                                                                                            217; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RATIUS NORVEGICUS (F
EUKARYOTA; METAZOA;
     18
333
121
27
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348
370
370 AA;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=BRAIN;
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OPRD_RAT
P33533;
                        DISULFID
                                                        CONFLICT
     CARBOHYD
                                                                                                         Query Match
Best Local
                 CARBOHYD
                                             CONFLICT
                                                                                      SEQUENCE
                                                                           CONFLICT
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                                                                                                                                                                                                                                                        SIMONIN F., BEPORT K., GAVERIAUX-RUFF C., MATTHES H., NAPPEY V.,
LANNES B., MICHELETTI G., KIEFFER B.;
"The human delta-optoid receptor: genomic organization, cDNA cloning,
functional expression, and distribution in human brain.";
MOL. PHARMACOL. 46:1015-1021(1994).
                                                                                                                                                                                                                                                                                                                                GRÂFHAM D.;
SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBU DATA BANKS.
SUBMITTED (FEB-1998) TO EMBL/GENBANSMITTER RELEASE BY REDUCING CALCIUM
TO CURRENTS AND INCREASING POTASSIDM ION CONDUCTANCE. HIGHLY
STEREOSELECTIVE. RECEPTOR FOR ENKEPHALINS
STEREOSELECTIVE. TO POTASSIDM SHORT STEREOSELECTIVE SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                           KNAPP R.J., MALATYNSKA E., FANG L., LI X., BABIN E., NGUYEN M., SANTORO G., VARGA E.V., HRUBY V.J., ROESKE W.R., YAMAMURA H.I.; "Identification of a human delta opioid receptor: cloning and
                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEMBRANE; GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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7 (POTENTAL).
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CYTOPLASMIC (POTENTIAL).
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                                               01-FEB-1995 (REL. 31, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DELTA-TYPE OPIOID RECEPTOR (DOR-1).
OPRDI OR OPRD.
                                    372 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PALMITATE
                                                                                                                            PRIMATES; CATARRINI; HOMINIDAE; HOMO
                                    PRT;
                                                                                                                                              SEQUENCE FROM N.A.
IISSUE-BRAIN CORTEX, AND STRIATUM;
MEDLINE; 94260835.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION; LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00001; 7tm_1; 1.
G-PROTEIN COUPLED RECEPTOR;
                                                                                                                                                                                                            expression.";
LIFE SCI. 54:463-469(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL009181; B1250368;
GCRDB; GCR_1017; -.
GCRDB; GCR_2055; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U07882; G497314; -.
                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U10504; G501145;
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                         JT 10
OPRD_HUMAN
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IRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 94322412.
ABOOD M.E., NOEL M.A., FARNSWORTH J.S., IAO Q.;
"Molecular cloning and expression of a delta-opioid receptor from rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FGIVRYTKMKTAINIYIFNLALADALATSILPFQSAKYLMETWPFGELLCKAVLSIDYYN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MFTSIFTLTMMSVDRYIAVCHPVKALDFRTPAKAKLINICIWVLASGVGVPIMVMAVTRP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MFTSIFTLTMMSVDRYIAVCHPVKALDFRTPLKAKIINICIWLLASSVGISAIVLGGTKV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                           LFANASDAYPS-A-CPSAGANASGPPGARSAS-SLALAIAITALYSAVCAVGLLGNVLVM 71
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FUKUDA K., KATO S., MORI K., NISHI M., TAKESHIMA H.;
"Primary structures and expression from cDNAs of rat opioid receptor
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. NEUROSCI. RES. 37:714-719(1994).

-!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM

-!- FUNCTION: INHIBITS NEUROPARASING POTASSIUM ION CONDUCIANCE. HIGHLY

STEREOSELECTIVE. RECEPTOR FOR ENKEPHALINS.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RDGA-VV-CMLQFPSP--SWYWDTVTKICVFLFAFVVPILLITVCYGLMLLRLRSVRLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSKEKDRSLRRITRMVLVVVGAFVVCWAPIHIFVIVWTLVDIDRRDFLVVAALHLCIALG
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6
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERLA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATIUS.
                                                                                                                                                                                                                                                                                                    Length 372;
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 3E, LAST ANNOMATION UPDATE)
DELIA-TYPE OPICID RECEPTOR (DOR-1) (OPICID RECEPTOR A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              320 YINSSLNPVLYAFLDENFKRCFRDFCFPIKMRMERQSTNRVRNT 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YANSSLNPVLYAFLDENFKRCFRQLCRKPCGRPDPSSFSRAREA 351
                     EXINITARITY.
PALMITATE (POTENITAL).
C -> F (IN REF. 1).
AR -> PG (IN REF. 1).
A -> P (IN REF. 1).
A -> R (IN REF. 1).
A -> R (IN REF. 1).
W; 4A57DD07 CRG32;
                                                                                                                                                                                                                                                                                                    Score 1612; DB 1; I
Pred. No. 1.27e-294;
                                                                                                                                                                                                                                                                                                                                                                        60; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372 AA
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
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NG108-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MFTSIFTLFMMSVDRYIAVCHPVKALDFRTPAKAKLINICIWVLASGVGVPIMVMAVTQP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | RDGA-VV-CTLQFPSP--SWXWDTVTKICVFLFAFVVPILIITVCYGLMLLRLRSVRLLS 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FGIVRYTKLKTATNIYIFNLALADALATSTLPFQSAKYLMETWPFGELLCKAVLSIDYYN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REDUDVIECSLQFPDDEYSW-WDLFMKICVFVFAFVIPVLIIIVCYTLMILRLKSVRLLS 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                             1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELIGIAR (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
EXTRACELIGIAR (POTENTIAL).
EXTRACELIGIAR (POTENTIAL).
5 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
6 (POTENTIAL).
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                                                                                                                                      PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
PFAM; PF00001; 7tm_1; 1.
G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; PHOSPHORYLAFION; LIPOPROTEIN; PALMITATE.
                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
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PALMITATE (POTENTIAL).
59F5EE50 CRC32;
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55; Mismatches
                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                        40449 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                            56.78;
                                                                               EMBL; D16348; G391865; -. EMBL; U00475; G514211; -. PIR; S34592; S34592. GCRDB; GCR_0638; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                              GCRDB; GCR_0805; -
                                                                                                                                                                                              214;
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OPRD_MOUSE
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01-0CT-1993 (REL. 27, CREATED) 01-0CT-1993 (REL. 27, LAST SEQUENCE UPDATE) 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE) DELTA-TYPE OPIOID RECEPTOR (DOR-1) (K56) (MSL-2).

372 AA.

PRT;

STANDARD;

P32300; 01-0CT-1993 01-0CT-1993

DEDE

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                                                                                                                                        "The delta-opioid receptor: isolation of a cDNA by expression cloning and pharmacological characterization."; PROC. NAIL. ACAD. SCI. U.S.A. 89:12048-12052(1992).
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BIDEGA T., CHIN H., KIM K., JUNG H.H., KOZAK C.A., KLBE W.A.;
"Regional expression and chromosomal localization of the delta opiate receptor gene.".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLUIAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
IN THE BASAL GANGLIA AND LIMBER RECEPTORS IN THE BASAL GANGLIA AND LIMBER RECONS.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 93391482.
KETIH D.E. JR., ANTON B., EVANS C.J.;
"Characterization and mapping of a delta opioid receptor clone from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G CALCIUM
HIGHLY
                                                                                                                                                                                                                               MEDLINE; 93110361.
PASNS C.J., KEITH D.E. JR., MORRISON H., MACENDZO K., EDWARDS R.H.;
"Cloning of a delta opicid receptor by functional expression.";
SCIENCE 258:1952-1955(1992).
                                                                                                                                                                                                                                                                                                                                                                       YASUDA K., RAYNOR K., KONG H., BREDER C.D., TAKEDA J., REISINE T.,
                                   MAMMALIA; EUTHERIA;
MUS.
                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning and functional comparison of kappa and delta opioid receptors from mouse brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 97001837.
ALKORTA I., LOEW G.H.;
"A 3D model of the delta opioid receptor and ligand-receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. H STEREOSELECTIVE. RECEPTOR FOR ENKEPHALINS.
                                                                                                                         GAVERIAUX-RUFF C., HIRTH C.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            PROC. NATL. ACAD. SCI. U.S.A. 90:6736-6740(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROC. NATL. ACAD. SCI. U.S.A. 90:9305-9309(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROC. WEST. PHARMACOL, SOC. 36:299-306(1993)
                               EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L07271; -; NOT_ANNOTATED_CDS.
EMBL; L11064; G348247; -.
EMBL; S65335; G442326; -.
EMBL; S66181; G435782; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complexes.";
PROTEIN ENG. 9:573-583(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L06322; G192943; -.
EMBL; L07271; -; NOT_ANNO
                                                                                                       MEDLINE; 93101664.
KIEFFER B.L., BEFORT K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3D-STRUCTURE MODELLING.
                MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR, S37807; S37807.
PIR, B48227; B48227.
GCRDB; GCR_0229; -.
GCRDB; GCR_0493; -.
                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                             93110361.
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                                                                                                                                                                                                                                                                                                                                      TISSUE=BRAIN;
MEDLINE; 93342064.
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L28144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKYLMETWPFGELLCKAVLSIDYYNMFTSIFTLTMMSVDRYIAVCHPVKALDFRIPAKAK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LINICIWVLASGVGVPIMVMAVTQPRDGA-VV-CMLQFPSP--SWYWDTVTKICVFLFAF 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 VVPILIITVCYGLMLLRLRSVRLLSGSKEKDRSLRRIIRMVLVVVGAFVVCWAPIHIFVI 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VWTLVDINRRDFLVVAALHLCIALGYANSSLNPVLYAFLDENFKRCFRQLCRTPCGRQEP 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
NOCICEPTIN RECEPTOR (CRPBAIN FO RECEPTOR) (KAPPA-TYPE 3 OPIDID RECEPTOR) (KOR-3) (ROR-C) (XORL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; METAZOA; CHORDATA; VERIEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATIUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 372;
                                                                                                                                            2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.62e-291;
51; Mismatches 46; Indels
            MGD, MGI:07438: OPRD1.
PROSITE: PS00237: G_PROTEIN_RECEPTOR; 1.
PFAM; PF00001; 77m_1; 1.
G-PROTEIN COUPLED RECEPTOR; TRANSMENERANE; GLYCOPROIEIN; PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
                                                                                                                                                                                                                                                                          6 (POTENTIAL).
EXIRACELLULAR (POTENTIAL).
7 (POTENTIAL).
                                                                                                EXTRACELLULAR (POTENTIAL)
1 (POTENTIAL).
                                                                                                                               CYTOPLASMIC (POTENTIAL).
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PALMITAIE (POIENTIAL).
514022F5 CRC32;
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Pred. No. 1.62e-291;
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STRAIN-WISTAR; IISSUE-BRAIN;
MEDLINE; 94215703.
                                                                                                                                                                                                                                                                                                                                                                                                                                             56.3%;
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18
33
121
333
372 AA;
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hes 206; Conser
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3CRDB; GCR_0842;
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OPRX_RAT
P35370;
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LIPID
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LACHOWICZ J.E., SHEN Y., MONSMA F.J. JR., SIBLEY D.R.;
"Mollecular cloning of a novel G protein-coupled receptor related to the opiate receptor family";
J. NEUROCHEM. 64:34-40(1995). THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLYL -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN SEVERAL BRAIN AREAS. -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. the WANG J.B., JOHNSON P.S., IMAI Y., PERSICO A.M., OZENBERGER B.A., EPPLER C.M., UHL G.R.; WATSON MIYATA T., HOUTANI T., SUGIMOTO I.; "CDNA cloning and regional distribution of a novel member of opioid receptor family."; IISSUE-HIPPOCAMPUS; MENG F., XIE G., ALFRED M., IHOMPSON R., HOVERSIEN M., SUBMITTED (JAN-1994) TO EMBL/GENBANK/DDBJ DATA BANKS. SEQUENCE FROM N.A. STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN; opioid receptor family."; FEBS LETT. 343:42-46(1994). splice variant."; FEBS LETT. 348:75-79(1994) G451844; -. G487965; -. G496220; -. EMBL; D16438; G533355; -. SEQUENCE FROM N.A. MEDLINE; 94298959. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE; 94307400. EMBL; U05239; EMBL; U01913; IISSUE=BRAIN; TISSUE=BRAIN;

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OPRX_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLPFQGTDILLGFWPFGNALCKTVIAIDYYNMFTSTFTLTAMSVDRYVAICHPIRALDVR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 ISSKAQAVNVAIWALASVVGVPVAIMGSAQV-EDEE-IECLVEIPAPQDY-WGPVFA-IC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 367;
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2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                  4 (POTENTIAL).
EXTRACELLUAR (POTENTIAL).
CYCOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLUAR (POTENTIAL).
7 (POTENTIAL).
7 (POTENTIAL).
7 (POTENTIAL).
BY SIMILARITY.
PALMITATE (POTENTIAL).
PALMITATE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63; Mismatches 61; Indels
                                                                                                                                                                   TRANSMEMBRANE, GLYCOPROTEIN;
1; PALMITATE.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
POTENTIAL.
POTENTIAL.
G -> R (IN REF. 2).
L -> V (IN REF. 2).
S -> P (IN REF. 2).
S -> T (IN REF. 3).
7 7FD40CCC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1473; DB 1; 1
Pred. No. 7.03e-266;
                                                                                                                                  PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1. PFAM; PF00001; 7tm_1; 1.
                                                                                                                                                                   G-PROTEIN COUPLED RECEPTOR; TR PHOSPHORYLATION; LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             40523 MW;
1, U07871; G606803; -.
1, L33916; G557200; -.
1, L24419; G51719; -.
1, S46238; S446238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 59.3%;
Matches 188; Conservative
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MRMERQSTNRVRNTVQD 366
                                                     GCRDB, GCR_0834; ...
GCRDB, GCR_0898; ...
GCRDB, GCR_1030; ...
GCRDB, GCR_1455; ...
GCRDB, GCR_1455; ...
GCRDB, GCR_1457; ...
GCRDB, GCR_1487; ...
                                                                                                                                                         HSSP; P34996; 1DDD.
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DOMAIN
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LIPID
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EMBL;
EMBL;
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HALFORD W.P., GEBHARDT B.M., CARR D.J.J.;
"Functional role and sequence analysis of a lymphocyte orphan opioid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MADLINE; 96387345.
MATTHES H.W.D., SEWARD E.P., KIEFFER B., NORTH R.A.;
"Functional selectivity of orphanin FQ for its receptor coexpressed
with potassium channel subunits in Xenopus laevis occytes.";
MOL. PHARMACOL. 50:447-450(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. NEUROIMMUNOL. 59:91-101(1995).

-!- FUNCTION: RECEPTOR FOR THE NEUROPEPTIDE NOCIPEPTIN/ORPHANIN FO.

HAS A POTENTIAL ROLE IN MODULATING A NUMBER OF BRAIN FUNCTIONS,

INCLUDING INSTINCTIVE BEHAVIORS AND EMOTIONS. THE ACTIVITY OF

THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAN Y.-X., CHENG J., XU J., ROSSI G., JACOBSON E., RXAN-MORO J., RSOOKS A.L., DEAN G.E., STANDIFER K.M., PASTERNAK G.W.; "Cloning and functional characterization through antisense mapping a kappa 3-related opioid receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MISDLINE, 95100967.
MISHI M., TAKEBUHMA H., MORI M., NAKAGAWARA K.I., TAKEBUCHI T.;
MISHI M., TAKEBUHMA H., MORI M., NAKAGAWARA K.I., TAKEBUCHI T.;
Structure and chromosomal mapping of genes for the mouse
kappa-opioid receptor and an opioid receptor homologue (MOR-C).";
BIOCHEM. BIOPHYS. RES. COMMUN. 205:1353-1357(1994).
            P35377; Q60645;
01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
NOCICEPTIN RECEPTOR (ORPHANIN FO RECEPTOR) (KAPPA-TYPE 3 OPICID
RECEPTOR) (KOR-3) (ORCC) (K3 OPIATE RECEPTOR)
                                                                                                                                                                             EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENIIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-CSPBL/GN; TISSUE-BRAIN;
YASUDA K., JONES E., REISINE T., BELL G.I.;
YABUDA K., JONES E., REISINE T., BELL G.I.;
SUBMITTED (JAN-1994); TO EMBL/GENBANK/DDBJ DAIR BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. PAN Y.-X., XU J., PASTERNAK G.W.; SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
367 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHARMACOL. 47:1180-1188(1995).
PRT;
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EMBL, D31667, G808874; -.
EMBL, D31666; G808874; JOINED.
EMBL, S791813; G1008982; -.
EMBL, U32932; G1464791; -.
EMBL, U32928; G1464791; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-357 FROM N.A. STRAIN-BALB/C; TISSUE-SPLEEN; MEDLINE; 95318231.
STANDARD;
                                                                                                                                       OPRL1 OR OPRL OR OOR.
                                                                                                                                                            (MOUSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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43 GAFLPLGLKVTIVGLYLAVCVGGLLGNCLVMYVILRHTKMKTATNIYIFNLALADTLVLL 102
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IRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             290 IHIFILVEALGSTSHSTAALSSYYFCIALGYINSELNPVIYAFLDENFKRCFRDFCFPIK 349
                                                                                                                                                                                                                                                                                                                                                                                            100 TLPFQGTDILLGFWPFGNALCKTVIAIDYXNMFTSTFTLTAMSVDRYVALCHPIRALDVR 159
                                                                                                                                                                                                                                                                                                                                                                                                                               160 ISSKAQAVNVAIWALASVVGVPVAIMGSAQV-EDEE-IECLVEIPAPQDY-WGPVFA-IC 215
                                                                                                                                                                                                                                                                                                                                                           SAFLPLGLKVTIVGLYLAVCIGGLLGNCLVMYVILRHTKMKTATNIYIFNLALADTLVLL 99
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      230 VEVEAEVIPVLIIIVCYTLMILKLKSVRLLSGSREKDRNLRRIIKLVLVVVAVFIICWTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 VQVFVLVQGLGVQPGSETAVAILRFCTALGYVNSCLNPILYAFLDENFKACFRKFCCASA
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P41146;
01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
NOCICEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR) (KAPPA-TYPE 3 OPIOID
                                                                                                                                                                                                                                                                                                                                            'n
                                                                                                                                                                                                                                                                                                                          Length 367;
                                              GCRUE; GCR_1728; -
GCRDB; GCR_1738; -
GCRDB; GCR_1731; -
MGD; MGI:97440; OPRL.
MGD; MGI:97440; TAM.
PROSITE; PS00237; Q_PROTEIN_RECEPTOR; 1.
PFRM: PP00001; 7tm_1; 1.
HSSP; P34996; 1DDD.
G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.

PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
                                                                                                                                                                                                                                                                                                                         Score 1471; DB 1; Length 36
Pred. No. 1.82e-265;
63; Mismatches 61; Indels
                                                                                                                                                 2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                   4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                  3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                 1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                              PALMITATE (POTENIIAL).
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3F472156 CRC32;
                                                                                                                                                                                                                    6 (POIENTIAL).
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                                                                                                                                                                                                                                                                               POTENTIAL.
POTENTIAL.
SI -> TV (I
U32930; G1464791; JOINED. U09421; G551485; -. U14165; G540093; -.
                                                                                                                                                                                                                                                                                                         40491 MW;
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59.3%;
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hes 188; Conservative
                                                                                                                                 3370
3370
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                         GCR_0891; -.
GCR_1715; -.
GCR_1716; -.
                                                                                                                                                                                                                                                                                                        367 AA;
                                                                                                              PHOSPHORYLATION; I
DOMAIN 1
TRANSMEM 48
DOMAIN 75
TRANSMEM 85
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DISULFID
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                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                  GCRDB;
GCRDB;
EMBL;
EMBL;
EMBL;
                           GCRDB;
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                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

LEE P.H., ZHU J., LIU-CHEN L., CHANG K.;

SUBMITTED (JAN-1996) TO EMBL/GENBARK/DDBJ DATA BANKS.

-!-ENGYTION: RECEPTOR FOR THE NUGROPEPTIDE NOCIPEPTIN/ORPHANIN FO.-

FAS A POTENITAL ROLE IN MODULATING A NUMBER OF BRAIN FUNCTIONS;

INCLUDING INSTINCTIVE BEHAVIORS AND EMOTIONS. THE ACTIVITY OF

THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADBNYINL

THIS TRUCKHOLD INCLUDING TO THE PROTEIN.
                                                                                                                                                                                         MOLLEREAU C., PARMENTIER M., MAILLEUX P., BUTOUR J.L., MOISAND C., FALLON P., CAPUT D., VASSARI G., MEUNIER C.; "ORLI, a novel member of the opioid receptor family. Cloning, functional expression and localization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
                                                                CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
L; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1465; DB 1; Length 370;
Pred. No. 3.15e-264;
65; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POIENTIAL).
6 (POIENTIAL).
EXTRACELLULAR (POIENTIAL).
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CYTOPLASMIC (POTENTIAL).
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PAINTER.
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PALMITATE (POTENTIAL).
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BE3C3E8F CRC32;
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CYTOPLASMIC (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 602548; -.
PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
PFAM; PF00001; 7tm_1; 1.
HSSP; P34996; 1DDD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40693 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION; LIPOPROTEIN;
DOMAIN 1 50 H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.6%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X77130; G471317; -. EMBL; U30185; G1144297; -. PIR; S43087; S43087.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 58.3%;
Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RECEPTOR) (KOR-3).
OPRL1 OR ORL1 OR OOR.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CI
                                                                                    PRIMATES; CAIARRHINI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCRDB; GCR_0987; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 AA;
                                                                                                                          SEQUENCE FROM N.A.
TISSUE=BRAIN STEM;
MEDLINE; 94185768.
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103 TLPPQGTDILLGEWPFGNALCKTVIAIDYYNMFTSTFILTAMSVDRYVAICHPIRALDVR 162 | 1:11| 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279 VQVFVLAQGLGVQPSSETAVALLRFCTALGYVNSCLNPILYAFLDENFKACFRKFCCASA 338
51 SAHISPAIPVIITAVYSVVFVVGLVGNSLVMFVIIRYTKMKTAINIYIFNLALADALVTT 110
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Feb 17 11:13:35 2000; MasPar time 27.84 Seconds 745.004 Million cell updates/sec Tabular output not generated. Run on:

>US-08-455-683-2 (1-380) from USO8455683.pep 2839 1 MESPIQIFRGDPGPTCSPSA.......RNIYQDPASMRDVGGMNKPV 380 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

179066 segs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptrembl9
1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle
9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified
13:sp\_vertebrate 14:sp\_virus

Mean 48.857; Variance 122.078; scale 0.400 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Pr	1.07e-252	10	.26e-1	4.66e-82	3.70e-74	1.12e-73	2.87e-71	3.79e-70	3.16e-68	4.56e-68	1.38e-67	4.15e-67	2.61e-66	9-6	3.77e-66	1.34e-63	2.78e-63	1.08e-61	3.24e-61	3.24e-61
scription	OPIOID RECEPTOR HOMOLO			DELTA OPIOID RECEPTOR/	GALANIN RECEPTOR TYPE	GALANIN RECEPTOR GALR2	CXCR4.	CHEMOKINE RECEPTOR CCR	CCR5 RECEPTOR (FRAGMEN	CCR5 RECEPTOR (FRAGMEN	RECEPTOR PROTEIN CKR3.	G PROTEIN-COUPLED RECE	CCR5 RECEPTOR (FRAGMEN	CHEMOKINE RECEPTOR CCR	CCR5 RECEPTOR (FRAGMEN	G PROTEIN COUPLED P2Y	CXC CHEMOKINE RECEPTOR	CHEMOKINE RECEPTOR.	MESENCHYME-ASSOCIATED	CHEMOKINE RECEPTOR CCR
A	573	042324	060733	264206	088854	043603	093247	077776	018770	015538	055169	589609	018772	054814	018771	057466	042445	018793	P79960	055193
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% Query Match	ີ. ດາ	٠	30.3	т С	÷	21.5	21.0	20.7		20.3		20.0	19.9	19.9	19.8	19.3			18.7	18.7
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	COUPLE ACTIN- N-LIKE RECEPT	G PROTEIN-COUPLED RECE GALANIN RECEPTOR TYPE P2Y5-LIKE RECEPTOR. CXCR4 GENE ENCODING RE	ECEPTOR TYPE EPTOR. KINE RECEPTO	ANGIOTENSIA RECEPTOR R LYMNOKININ RECEPTOR. GALANIN RECEPTOR TYPE BOMBESIN RECEPTOR SUBT	OMATOSTATIN RECEPTO HEMOKINE (C-C) RECE EUROMEDIN B RECEPTO NGIOTENSIN II RECEP-
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## ALIGNMENTS

		NEOPTERYGII; NOIDEA;	.E.; Y).	w	110	170	228	288	347
		ERY JA;	A H	Gaps					
		GII; NEOPTER CYPRINOIDEA;	RODRIGUEZ Y SIMILAR N.	, <b>,</b> 4	LPFC  - -  MPFC	PIK?  :   PLK?	FAE 	EETI  :	RADO RES
		, N RIN	DRI SIM	373	TST  :  TTT	FRT 	CVE	PIH.	FRTH :: IKMI
		GII	, RO (BY EIN.	ength Indels	ALA  -   ALV	ALE   :	TKI HA	CWT	CLP CFP
	<b>⊆</b>	rery 3S;	E., NKS. IN (1	Length Indel	ALAI       ALAI	HPVF    :	NDTV 	EII FII	PRDE
	DATE) UPDATE	NOP! ORMI	MALVAR F., R AATA BANKS. PROTEIN (BY GLYCOPROTEIN		FNL	AVCI AVCI	W-YV YSWW	W.A.	KRCI HHHH KRCI
, i	ADA V UP	ACTI	-MAI DATA E PR GLY 332;	3 13 2-25	IXI 	RYI      RYI	∃. ∃. ∃.	V. 15'	ENF 
3 A.A	CEL	NIO) A; A YPRJ	CIA: BJ I RANI RANI CRC	DI . 076 ches	TAT 	MSVI         SVI	CKFF 	ITER	AFLE 
37.	ED) SEQUENCE UPDATE ANNOTATION UPDA	RAT.	R., GARCIA-MAL NBANK/DDBJ DATA RAL MEMBRANE PR EPTOR, 1.	Score 1687; DB 13; Pred. No. 1.07e-252; 62; Mismatches 42;	KLK  :  KMK	LIM	-CM -CM -CM	MRR:      - -   LRR	ALY VLY
÷	SEC ANN	EBRA RTEE HYSI	R., BANK AL N PTOF SMEN	e 16 Mis	VRYI :    IRYI	SIFI	VITIN : IVO'	ORN ORN	SLNP
PRT	CREATED LAST SEG LAST AND	(Z) (E) (TOP)	HO GEN GEN EGEN RAN ECE	cor red 2;	YGV : : FVI	MET:	TNO HED	SKE  :  SRE	E NE NE NE NE NE NE NE
	06, C 06, I 07, I	E. FISH) CDATA; OSTAR DANIO	TIEN TINT TINT TINT TINT TINT TINT TINT		ILVM ILVM	OYYN 	TRV  :  STKV	LSG 	-GY LGY
Υ;	. 06, . 06, . 07,	GUE RAFI ORDZ 1 OS 1 DZ	SARNON: ON: OTE: OTE:	4.6. 9.89 9.90	LGN)	IAI  :  ISI	IMA\	SVRI       SVRI	LHRI : : FCI?
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IMI	IMBI IMBI IMBI	HON TO ( ZOA; ZOA; SORI	.A. NZAI 1997 100 E12 E12 7; G	lty nser	ZICV  :   VFV	SLLC ::	AVGV :  : SVGI	I I I	VIA
PREJ	GEN GENERAL	TOR RER ETA UTEI RASI	A., GONZA (SEP-19) (SEP-19) (D1596; E. PS00237; (COUPLED 373 AA.	lar: Cor	LYS'  - -  - -	PFG! 	LSSZ  :  LASS	CYGI  -  CYTI	KNPE : STA-
	01-JUN-1998 01-JUN-1998 01-AUG-1998	OPICID RECEPTOR HOMOLOGUE.  BRACHYDANIO RERIO (ZEBRATSH) (ZEBRA DANIO).  BUKARYOTA: METAGOA: CHORDATA: VERTEBRATA; ACTINOPTERYGII;  TELEOSTEI: EUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; CYPRI	113 BARRALLO A., GONZALEZ-SARMIENTO R., GARCIA-MALVAR F. BARRALLO A., GONZALEZ-SARMIENTO R., GARCIA-MALVAR F. SUBMITTED (SER-1997) TO EMBL/GENBANK/DDBJ DATA BARKS 1- SUBGELLULAR, LOCATION: INTEGRAL MEMERANE PROTEIN EMBL; AJ001596; E1217996; . RENGITE, REGOUZ37; G.PROTEIN RECEPTOR; 1. G.PROTEIN COUPLED RECEPTOR: TRANSMEMBRANE; GLYCOPROT: SEQUENCE 373 AA; 42520 MW; E900D477 CRC32;	simi 36;	IAISITALYSVICVVGLLGNILVMYGVVRYTKLKTATNIYIFNLALADALATSTLPFGST  ::    :   :	XXLMNTWPFGELLCKVVIAIDYYNMFTSIFTLTMMSVDRYIAVCHPVRALEFRTPIKAKI 	INVCIWILSSAVGVPIMIMAVIRVTNQNTTV-CMLKFPDPDW-YWDTVIKICVFIFAFVV   :   :  :  :  :  :  :  :  :  :  :  :	PVLVIIIOYGLMILRLKSVRLLSGSKEKDRNMRRITRWYLVVVAAFIICWTPIHIFIIBK    : :	ILVDINQKNPFVIASWHLHRT-GYTNSSLNPVLYAFLDENFKRCFRDFCLPFRTRADQSN     :: : ::
HΩ.	6 Z Z C	YORK	SEQUENCE BARRALLO SUBMITTED -1- SUBCE EMBL; AJO PROSITE; G-PROTEIN SEQUENCE	tch al 9 2(	IAIS   ::   IPV	KY EN	INVC INIC	PVLA         PVLJ	TLVI :-
1 057585 057585	3 P.	MACH MAR MAR MEDO MEDO MEDO	NRRA NRRA IBMI S IBL: NOSI	Locales	51	1 8 1	171	223	289
틷	2000	10 H H H H H	S S S S S S S S S S S S S S S S S S S	Ouery Match 59.4%; Best Local Similarity 65.6%; Matches 206; Conservative		<b>⊢</b> ⊢		(4 (4	(4 (4
RESULT ID O	2555	00000	SO WE CREATED SO WE WAS A SO W	ÕÃĬ	Db	DP	QQ OX	Db	Db Qy

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FITVARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUKARYOTA; METAZOA; CHÖRDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; COBITOIDEA;
CATOSTOMIDAE; CATOSTOMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DARLISON M.G., HARVEY R.J., GRETEN F.R., KREIENKAMP H.J., ZWIERS H., STHMER T., LEDERIS K., RICHTER D.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

-1. SUBGELLULIAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

EMBL; Y10904; E1169530; -.
PROSITE; PRO127; G.PROTEIN_RECEPTOR; I.

FRAM; DF00011; 7tm_1; 1.

FRAM; DF00011; 7tm_1; 1.

FRAM; DF00011; 7tm_1; 1.

FRAM; DF00011; 7tm_1; 1.

FRAM; DF00TEIN COUPLED RECEPTOR; I.

FRAM; DF00TEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSSRDSTDEQDKTPVIIAIIITTLYSIVCVVGLVGNVLVMYVIIRYTKMKTAINIYIFNL 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEYSWWDLFMKICVFVFAFVIPVLIIIVCYTLMILRLKSVRLLSGSREKDRNLRRITKLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
&
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDAIE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
021.01D RECEPTOR, KAPPA 1 (KAPPA OPIOID RECEPTOR) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FKRCFREFCVPSPSVLDLQNSTRNSNPQCEGQSSGHKVDRNNRQV 383
                                                                                                                                                                                                                                                                                                                     LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1652; DB 13;
Pred. No. 8.81e-247;
63; Mismatches 60;
                                                                                                                                                                                                                             383 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                        CATOSTOMUS COMMERSONI (WHITE SUCKER)
                                                                                                                                                                                                                                                                                             CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA; CHORDATA; VERTEI
SCIUROGNATHI; MURIDAE; MURINAE; MUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                      01-JAN-1998 (TREMBLREL. 05,
01-JAN-1998 (TREMBLREL. 05,
01-NOV-1998 (TREMBLREL. 08),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 58.2%;
Local Similarity 62.0%;
Nes 214; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                             PRELIMINARY;
                                                                || || :::| |:
357 TNRVRNTVQDPASM 370
                              348 LNRARNATREPUSV 361
                                                                                                                                                                                                                                                                                                                                                                                         MU-OPICID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. GRANDY D.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=CNS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Q60733
Q60733;
                                                                                                                                                                                              LT 2
042324
042324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40
                              g
                                                                                                                                                                                                                                   HD DDH BERNAR BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
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MUS MUSCULOS (MOUSE).

EUKARYOTA; METAZOA; CHORDAIA; VERIEBRAIA; MAMMALIA; EUTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUS MUSCULUS (MOUSE).
EUKARXOIA; METAZOA; CHORDAIA; VERIEBRAIA; MAMMALIA; EUTHERIA; RODENTIA;
                                                                                                                                                                                                                                                                                                                                    87 YIKMKTAINIYIFNLALADALVITIMPFQSAVYLANSWPFGDVLCKIVISIDYYNMFISI 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 IFTLIMMSVDRYIAVCHPVKALDFRTPLKAKIINICIWLLASSVGISAIVLGGTKVREDV 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                             1 YTKMKTATNIYIFNLTLADALVTTTMPFQSAVYLMNSWPFGDVLCKIVISIGYYNMFTSI 60
SUBMITTED (NOV-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

EMBL; U16998; G555337; -.

MGD; MGI:97439; OPRKI.

PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.

PRAM; PF00001; 7tm_1; 1.

G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GIXCOPROTEIN.
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                1 IFTLIMMSVDRYIAVCHPVKALDFRTPAKAKLINICIWVLASGVGVPIMVMAVTQPRDGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 -LV-CMLQFPSP--SWYWDTVTKICVFLFAFVVPILITTVCYGLMLLRLRSVRLLSGSKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 FILIMMSVDRYIAVCHPVKALDFRTPLKAKIINICIWLLASSVGISAIVLGGTKVRE
                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.3%; Score 662; DB 11; Length 119;
larity 69.9%; Pred. No. 4.66e-82;
Conservative 17; Mismatches 15; Indels
                                                                                                                                                                                                                             Length 117;
                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                         Score 860; DB 11; I
Pred. No. 2.26e-114;
1; Mismatches 1;
                                                                                                                                                                                     13070 MW; FCCF68E1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             371 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DULT 5 O88854 PRELIMINARY; O88854 C1-NOV-1998 (TREMBIREL. 08, C 01-NOV-1998 (TREMBIREL. 08, L GALANIN RECEPTOR TYPE 2.
                                                                                                                                                                                                                           30.3%;
larity 98.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                    117
                                                                                                                                                                  117 1
117 AA;
                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 115; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity
Matches 86; Conser
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3

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10;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273 TKLVLVVVAVFICWTPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLNPVLYF 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 FILNLGVADLCFILCCVPPQATIYTLDDWVFGSLLCKAVHFLIFLTMHASSFTLAAVSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YIFNLALADA-LVTTTMPFQSAVXLMNSWPFGDVLCKIVISIDYYNMFTSIFTLTMMSVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RYLAIRYPMHSRELRTPRNALAAIGL-IWGLAL-L-FSGPYLSYYSQSQLANLIVCHPAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAP--RRRA--MDLCIFVFSYLLPVLVLSLTYA-RILHYLWRTVDPVAAGSGSQRAKRKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 PDDEYSWWDLFMKICVFVFAFVIPVLIIIVCYTLMILR-L-KSVRLLSGSREKDRNLRRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRMIVIVAVLFCLCWMPHHALILCVWFGRFPLTRAIYALRILSHLVSYANSCVNPIVYAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGSDSQGAEDSSQEGGGGQPEAVLVPLFFALIFLVGAVGNALVLAVLLRGGQAVSTINL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,
D
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"Galanin Receptor Type 2 (GalR2) from Human and Mouse: Genomic Cloning, Chromosomal Localization, Functional Expression, Gq Dependent Signal Transduction, and Expression Pattern.";
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF040630; G2921760; -.
                                                                                                                                                                                                                                                                                                                                                  21.6%; Score 613; DB 11; Length 371;
larity 29.6%; Pred. No. 3.70e-74;
Conservative 10%; Mismatches 111; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GalR2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZHANG
                                                                SEVUENCE .....
STRAIN-195/SV.;
KOLAKOWSKI L.F. JR., BROUSSARD S.R.;
KOLAKOWSKI L.F. JR., BROUSSARD S.R.;
Galanin Receptor Type 2 (GalR2) from Human and Mouse: Genc Cloning, Chromosomal Localization, Functional Expression, C Dependent Signal Transduction, and Expression Pattern.";
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBU DATA BANKS.
EMBL; AF042784; G3642918; -.
EMBL; AF042784; G3642918; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOOMQUIST B.T., BEAUCHAMP M.R., ZHELNIN L., BROWN S.-E. GORE-WILLS A.R., GREGOR P., CORNEIELD L.J., "Cloning and expression of the human galanin receptor Gallochem, BIOPHYS. RES. COMMUN. 243:474-479(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
RATHAGLINO P.M., IBEN L.G., LI H., BAKER E.
MCGOVERN N. AHLLE C.D., SUTHERLAND G.R., IISMAA T.P.
DICKINSON K.E.J., ANTAL ZIMANYI I.;
SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : :|:: || : | ::: || LDENFKRCFRDECFPIKMRMERQSTNRV 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSKHFRKGFRKICAGLLRRAPRRASGRV 321
   MURINAE; MUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06,
06,
08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
GALANIN RECEPTOR GALRZ.
SCIUROGNATHI; MURIDAE;
                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A.
98153789.
                                                       FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OR GALR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM MEDLINE; 98153
                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         л
043603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   043603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GALNR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C
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TELEOSTEI; EUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; CYPRINOIDEA;
CYPRINIDAE; CYPRININAE; CYPRINUS.
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PVIITAVYSVVFVVGLVGNSLVMFVIIRYTKMKTATNIYIFNLALADA-LVTIIMPFQSA 117
                                                                                                                                                                                               IYTLDGWVFGSLLCKAVHFLIFLTMHASSFTLAAVSLDRYLAIRYPLHSRELRTPRNALA 144
                                                                                                                                                                                                                                                                                                                                                TDKYRLHLSIADLLFVLTLPF-WAVDAASGWHFGGFLC-VTVNMIYTLNLYSSVLILAFI 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUJIKI K., NAKAO M., SHIN D., YANO T.;
"CDNA clothing of a carp homologue of mammalian CXCR4.";
"CDNA clothing of a carp homologue of mammalian CXCR4.";
SUBMITTED (MAR-1998) TO EMBL/GENBANKDDBJ DATA BANKS.
-!- SIBCELLULAR LOCATION: INIEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; AB012310; D103763; --
PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
FORDIN: CAPOTEIN COUPLED RECEPTOR; 1.
SEQUENCE 353 AA; 39633 MW; 23DD5347 CRC32;
                                                                                                   Gaps
                                                                                                                                25 AVIVPLLFALIFLVGTVGNTLVLAVLLRGGQAVSTTNLFILNLGVADLCFILCCVPFQAT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                              LPVLVLGLTYA-RTLRYLWRAVDPVAAGSGARRAKRKVTRMILIVAALFCLCWMPHHALT
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                                                                                                                                                                                                                                                                                            177 IINICIWLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDEYSWWDLFMKICVFVFAFV
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                                                                   Length 387;
                                                                                                  Indels
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LAST ANNOTATION UPDATE)
                                                                Score 610; DB 4; Le
Pred. No. 1.12e-73;
99; Mismatches 99;
                                   E7A343C3 CRC32;
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EMBL; AF058762; G3170599; -.
EMBL; AF042782; G3642914; -.
SEQUENCE 387 AA; 41700 MW;
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31.4%;
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EUKARYOIA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALLA; EUTHERIA; PRIMATES;
CATARRHINI; CERCOPITHECIDAE; CERCOPITHECINAE; CERCOCEBUS.
LOFP-DDEXSWWDLFMKICVFVAFAFVIPVLIIIVCYTLMILREKSVRLLSGSREKDRNLR 270
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"Natural infection of a homozygous delta 24 CCR5 red-capped mangabey with a R2b-tropic simian immunodeficiency virus.";

J. EXP. MED. 0:0-0-(1998).

ENRI, AF084604; 63694849; -.

SEQUENCE 352 AA; 40475 MW; 6649F573 CRC32;
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                                                                                                                                                                                              | ::|: |:||| |||:| : ||:|| ||:|| ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:|| : ||:||
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VFVFAFVIPVLIIIVCYTLMILRIKSVRLLSGSREKDRNLRRITKLVLVVVVAVFIICWTP
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Pred. No. 3.79e-70;
98; Mismatches 98; Indels 16;
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01-JAN-1998 (TREMBLREL. 05,
01-NOV-1998 (TREMBLREL. 08,
CCR5 RECEPTOR (FRAGMENT).
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01-NOV-1998 (TREMBLREL. 08,
01-NOV-1998 (TREMBLREL. 08,
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1D 018770
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DT 01-JAN-1
DE CCR5 REC
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SEQUENCE FROM N.A.
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STRAIN-MACCES-140A;
SHANG L., CARRUTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,
HO D.D.;
ALDS RES. HUM. RETROVIRUESS 0:0-0(1997).
ALDS RES. HUM. RETROVIRUESS 0:0-0(1997).
BMBL, AF011584, G2205194; -.
PFAM. PF00101; 7tm_1; 1.
NON_TER 352 AA; 40523 MW; FIC10E99 CRC32;
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20.3%; Score 575; DB 4; Lei
Best Local Similarity 28.9%; Pred. No. 4.56e-68;
Matches 87; Conservative 100; Mismatches 98;
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Pred. No. 3.16e-68;
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ZHANG L., CARRUTHERS C.D., HE T., HUANG Y.,
AD D.,
AIDS P.S. HUM. RETROVIRGES 0:0-0(1997).
EMBL; AF011516, G2305190; -.
EMBL, AF011516, G2305180; -.
EMBL, AF01154, G2305186; -.
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RECEPTOR PROJECTOR (RAT).
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
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HARRINGTON P.M., NEWTON D.J., COLEMAN J.W., FLANAGAN
BUBLITIED (JAN.1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; Y134(0): R1247073; -
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EQUINE HERPESYIRUS TYPE 2 (EHV-2).
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAO Y., WANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BANKS
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
CATARRHINI; HOMINIDAE; PAN.
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Larity 28.2%; Pred. No. 2.61e-66;
Conservative 100; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-86/67;
STRAIN-86/67;
TELFORD E.A.R.;
SUBMITTED (FEB-1995) TO EMBL/GENBANK/DDBJ DATA
EMBL; U20824; 6695251; -.
EMBL; U20824; 6695173; -.
PFAM; PF00001; 7tm_1; 1.
STOTIENCE 383 AA; 43667 MW; 60F5BFD4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      352 AA; 40598 MW; A9BF8EDF CRC32;
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                                                                                                                                                                 MEDLINE; 95302501.
TELEORD E.A., WAISON M.S., AIRD H.C., PE
"The DNA sequence of equine herpesvirus
J. Mol. BIOL. 249:520-528(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HO D.D.;
BOX SES, HUM. RETROVIRUSES 0:0-0(1997)
EMBL; AFOIL541; G2305200; --
PFAM; PF00001; 7tm_1; 1.
NON_TER 352 352
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larity 31.3%;
Conservative
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018772 O18772;
01-7AN-1998 (TREMBLREL: 0
01-5AN-1998 (TREMBLREL: 0
01-NOV-1998 (TREMBLREL: 0
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Best Local Similarity
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Matches 85; Conser
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                                                           [2]
SEQUENCE FROM N.A.
                                               FROM N.A.
[1]
SEQUENCE 1
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RATIUS NORVEGICUS (RAI).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURINAE; RATIUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S., XIA Y., FENG L., SONNTAG M.K., W.J., HARRISON J.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 IITAVYSVVFVVGLVGNSLVMFVIIRYTKMKTATNIYIFNLALADALVTTHMFQSAVYL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 YDIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLLV 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LWNEWGFGHCMCKMLSGLYYLALYSEIFFIILLTIDRYLAIVHAVLALRARTVTFAIITS 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 IHI-FIL-V-EAL-G-STSHSTAALS-SYYFCIALGYINSSLNPVLYAFLDENFKRCFRD
                                                                                                                                                                330 VFVFAFVIPVLIIIVCYTLMILRIKSVRLLSGSREKDRNLRRITKLVLVVVAVFICWIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IITWGFAVLAALPEFIFHES--QDNFGDLSCSPRYPEGEEDSWKRFHALRMNIFGLALPL
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                                                                                                                  RIVIFGVVISVITWVVAVFASLPGIIFIRSQ-KEGLHYI-CSSHFPYSQYQFWKNFQILK
                                                                                                                                                                                                                                                                IVILGLVLPLLVMVICYS-GIL--KT--LLRCRNEKKRH-RAV-RLIFTIMIVYFLFWAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 HSTFLETSCOOSIHLDLAMQVTEVITHTHCCINPIIYAFVGERFRKHLRLF 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.9%; Score 565; DB 11; Length 359; Larity 30.9%; Pred. No. 1.81e-66; Conservative 93; Mismatches 90; Indels 1
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JIANG Y., SALAFRANCA M.N., ADHIKARI;
DEFIBERE C.M., PENNELL N.A., STREIT;
J. DEVOLOMMUNOL. 0:0-0(1999).
EMBL; AF003954; G2897073; -..
SEQUENCE 359 AA; 41643 MW; CIFC7.
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PAN TROGLODYTES (CHIMPANZEE)
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01-JAN-1998 (TREMBLREL. 05,
01-JAN-1998 (TREMBLREL. 06,
01-NOV-1998 (TREMBLERL. 08,
CCR5 RECEPTOR (FRAGMENT).
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tes 90; Conser
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SEQUENCE FROM N.A.
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01-JUN-1998
01-JUN-1998
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CATARRHINI; HOMINIDAE; PAN.
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                                                                                                     WANG
                                                                                                     CAO Y.,
                                                                                                                    HO D.D.;

AIDS RES. HUM. RETROVIRUSES 0:0-0(1997).

EMBL; AF011539; G2305196; -.

PFAM, PF00001; 7tm_1; 1.

NON_TER 352 A5.

SEQUENCE 352 AA; 40466 MW; D52C67E1 CRC32;
                                                                                                     ZHANG L., CARRUTHERS C.D., HE T., HUANG Y.,
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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

February 17, 2000, 10:09:49; Search time 1154.67 Seconds (without alignments) -2629.655 Million cell updates/sec US-08-455-683-11 1000 1 AAGAAGCAAAATCAGTAATC......CCAGTATGACTAGTCGTGGA 1000 1642386 821193 seqs, -1518192014 residues OM nucleic - nucleic search, using sw model pass the threshold

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# 50: gb\_pl3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	79 Homo sapi	4 K	17298 Human	053 Humar	9600	60 нишаг	130 Homo	092 Cavi	Su	U16998 Mus musculu	g	attus no	S77869 kappa opioi	A68828 Sequence 5	E08874 cDNA coding	L11065 Mouse kappa	D16829 Rattus norv	at kap	L22536 Rattus norv	tat mR	attus	attu	appa-op	SSS	A38528 Sequence 1	dinence 3	on	ns wnscn	Touse delt	tat mRN	attus	erta	S66181 delta opiat	erta	louse	at mu	attus	attus n	kat mRN	U02083 Rattus norv	attus nor	S77863 mu-opioid r	appa opi	L25119 Human Mu op
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### ALIGNMENTS

RESULT 1 HUMOPRK1A LOCUS	HUMOPRKIA 455 bp DNA PRI 07-JAN-1995
DEFINITION	Homo sapiens (clone hSR4-1) kappa opioid receptor (OPRK1) gene,
ACCESSION	complete exon. L26079
VERSION	L26079.1 GI:416143
KEYWORDS	OPRK1 gene; kappa opioid receptor.
SOURCE	Homo sapiens (tissue library: Stratagene 946203; lambda) male
	placenta DNA.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

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EDAQLEPAHISPAIPVIITAVYSVVEVVĞLVONSLVMEVIIRYTKMKTATNIYIFNLA
TADALVATTAPPÇSYYLMINSPERGYPUCKIYISIDEYNMETSETFLIAMSYDERIAV
CHPYKALDFRAPLAKINICIMLISSSVGISALVLGGTKVBDVDVIECSLOFPDD
YSWADLFMILOYFIFAFVIPVLIIIVCYTLMILARSVRLLSGSREKDRNLRRITRLY
LVVRAYEVVCWYPIHIPILVBALGSTGHSTALSSYYFCIALGYTNSSLNPILYAFLD
THERREPERFERFERFERFYTRYTVQDPAILEDDGMNRPV"

337 c 283 g 286 t
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                WO 9601898-A 1 25-JAN-1996;
                                                                                                                                                                                     /protein_id="CAA03102.1"
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                                                                                                /organism="unidentified"
/db_xref="taxon:32644"
                                                                                                                                    1. .>1142
/note="unnamed protein
       Patent: WO your.
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Location/Qualifiers
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1 (bases 1 to 455)
Yasuda,K., Espinosa,R.III., Takeda,J., Le Beau,M.M. and Bell,G.I.
Localization of Kappa opioid receptor gene to human chromosome band
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Kieffer, B. and Simonin, F.
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 455;
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                                                                                                                                                                                     /sex="male"
/tissue_type="placenta"
/tissue_lib="stratagene 946203; lambda"
/map="8q11.2"
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                                                                                                                                                                                                                                                                                                                                                                                                              45.5%; Score 455; DB 9; Le
ilarity 100.0%; Pred. No. 3.9e-246;
Conservative 0; Mismatches 0;
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1. .455
/organism="Homo sapiens"
/db_xref="taxon:9606"
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A48343
A48343.1 GI:2302133
                                                                                                                                                                                                                                                                                         101. .453
/gene="OPRK1"
/note="G00-132-651"
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                                                                                                                                                                                                                                              /gene="OPRK1"
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l (bases 1 to 1154)
Simonin, retaining Hominidae; Homo.
Simonin,F., Gaveriaux-Ruff,C., Befort,K., Matthes,H., Lannes,B.,
Micheletti,G., Mattei,M.G., Charron,G., Bloch,B. and Kieffer,B.
Kappa-Opioid receptor in humans: cDNA and genomic cloning,
Chromosomal assignment, functional expression, pharmacology, and
expression pattern in the central nervous system
Proc. Natl. Acad. Sci. U.S.A. 92 (15), 7006-7010 (1995)
                                                                                                                                                                                                                                                                HSU17298 1154 bp mRNA PRI 14-JUL-1995
Human kappa opioid receptor (hKOR) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolation of a human kappa opioid receptor cDNA from placenta Biochem. Biophys. Res. Commun. 202 (3), 1431-1437 (1994) 94338360
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
     INGGGGANGIGCIGIGCAAGANAGIAANITICCANTGATIACIACAACANGITCACCAGCA
                                                            814 ICTICACCTIGACCAIGAFGAGGGGGACCGCTACATTGCCGTGTGCCCCCGTGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1294 CAGCIGCICICCCCAGCIAITACITCTGCAICGCCITAGGCIAIACCAACACAGAGCCGA
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                                       TCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTGTGCCGACCCGTGAAGG
                                                                                                       CTTTGGACTTCCGCACACCCTTGAAGGCAAAGAICATCAATATCTGCATCTGGCTGCTGT
                                                                                                                                                                                                                                                                                                                                     1054 TGAAGAICTGGGTCTTCAICTTTGCCTTGTGATCCCTGTCGTCAICATCAICGTCGGCT
                                                                                                                                                                                                                                                                                                                                                                                  ACACCCTGATGATCCTGCGTCTCAAGANNGTCCGGCTCCTTTCTGGCTCCCGAGAAAG
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                                                                                                                                        874 CTTIGGACTICCGCACACCCTIGAAGGCAAAGAICATCAATATCIGCATCIGGCTGCIGI
                                                                                                                                                                          CGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAAGTCAGGGAAGGTGTCG
                                                                                                                                                                                                            934 CGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAAGTCAGGGAAGACGTCG
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Mansson, E., Bare, L. and Yang, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 (bases 1 to 1154)
Kieffer, B.
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                                                     in lambda dash and cDNA in lambda
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   976
                                                                                                                                                                                                                                            (OPRK1) mRNA
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                                                                                                                                                                                                                          22-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 1604)

Zhu,J., Chen,C., Xue,J.-C., Kunapuli,S., Deriel,J.K. and Liu-Chen,L.-Y.

Clouing of a human .kappa. opicid receptor from the brain Life Sci 56, 201-207 (1995)

Location/Qualifiers
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 CAGCIGCICICICCAGCIATTACIICIGCAICGCCIITAGGCIATACCAACAGTAGCCIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              634 GATACACAAAGATGAAGACAGCAACCAACATTTACATATTAACCTGGCTTTGGCAGATG
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                                   ATCCCATICITCIACGCCTTICTTGAIGAAACTTCAAGCGGIGITTCCGGGGACTICTGCT
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                                                                                                                                                                                                                                                                                                          OPRKI gene; kappa opioid receptor; opioid receptor. Homo sapiens (clone d2-115) (tissue library; genomic and cDNA in lambda ZAPII) fetus brain cDNA to mRNA.
                                                                                                                                                                                                                                         d2-115) kappa opioid receptor
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Pred. No. 4.6e-237;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="kappa opioid receptor"
/protein_id="AAA63906.1"
/db_xref="G1:722618"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="GDB:G00-132-651"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="d2-115"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="brain"
/tissue_lib="genomic
                                                                                                                                                                                                                          mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="fetus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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/gene="OPRK1"
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/gene="OPRK1"
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ilarity 99.1%;
Conservative (
                                                                                                                                                                                                                         1604 bp
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                                                                                                                        L37362.1 GI:722617
                                                                                                     TICCACTGAAGAIGAG 895
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//Translation="MESPIQIFRGEPGPTCAPSACLPPNSSAWFPGWAEPDSNGSAGS
EDDOLEDAHIGSALIVAYSVYVYVGIVOSIVAWITYTKWITKYTRIVIA
ELDALVYTTURFQSYYVIMOSWFFGDVLCK TVISIDYYNMETSIFTLENLA
ELDALVYTTURFQSYYVIMOSWFFGDVLCK TVISIDYYNMETSIFTLENMSVDFYIAV
CHPVKALDFRTPLKAKIINICIWLLSSSVGISAIVLGGTKVREDVDVIECSLQFPDDD
TVSWDDLFWRICVFIFAAVIPVLIIVOYTLMINIKKSYNLESGSREKDRNLRRITRLV
IVVVANFVVOWTPIHFILVDRALGSTSHSTAALSSXYFCIALGYTNSELNPILYAFLD
BNFKRCFRDFCFPLKMRMERQSTSRVRUVQDPAYLRDDGMNKPV"
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Submitted (20-JUN-1994) Erik Mansson, Molecular Biology, Ohmeda,
PPD, 100 Mounatain Avenue, Murray Hill, NJ 07974, USA
Location/Qualifiers
                                                                                                                                                         916
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ATCGCAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGTGGCAGTCTTCGTCGTCT 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota, Matazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1182)
Mansson,E., Bare,L.A. and Yang,D.
Isolation of a human kappa opioid receptor cDNA from placents.
Biochem. Biophys. Res. Commun. 202, 1431-1437 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                              22-AUG-1994
cds.
                                                                           GCTGGACTCCCATTCACATATTCATCCTGGTGGAGGCTCTGGGGGAGCACCTCCCACAGCA
                                                                                                                  CAGCTGCTCTCCCAGCTATTACTTCTGCATCGCCTTAGGCTATACCAACAGTAGCCTGA
                                                                                                                                        ATCCCATTCICTACGCCTTTCTTGATGAAACTTCAAGCGGTGTTTCCGGGACTTCTGCT
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100.0%; Pred. No. 5.5e-189;
iive 0; Mismatches 0;
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/db.xref="taxon:9606"
/clone="phKl.3"
/tissue_type="placenta"
14. .1156
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/product="kappa opioid re
/protein_id="AAA20985.1"
/db_xref="GI:532060"
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Best Local S
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AUTHORS
TITLE
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VERSION
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HSU11053
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EDAQLEPAHISPALWAYSVYFYGLVOSIVAWFYTETKATKKITATRIXITENLA
EDAQLEPAHISPALWATSVYFYGLVOSIVAYOMYSVARFYSITTLIMASVDRIDA
EDALVYTTAMPROSTYVIMNSWPFGVVLCKYVISIDYYNMFTSIFTLIMASVDRIZIA
CHPVKALDFRIPLKAKIINICIWLLSSSVGISALVLGGTKVREDVUVIECSLQFPDDD
SYMDLEMRICVFIFARPIYDLIIVOYTLMILIKKSVYLEGSSREKDRNLRRITRLV
IVVVVAYPVVCWTPHIFILVBALGSSTSHSTAALSSSYFFCIALGYTNSRINFIKAY
ENFRKCFRDFCFPLKMRMERQSTSRVRUYQDPAYLRDIDGMNKPV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
      Direct Submission
Submitted (18-NOV-1994) Brigitte Kieffer, Ecole Superieure De
Biotechnologie De Strasbourg, Boulevard Sebastien Brandt, IllKirch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          676
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                                                                                                                                                                                                                                                                                                /note="G-protein coupled; transmembrane protein"/codon_start=1
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                                                                                                                                                                                                                                                                                                                                  /product="kappa opioid receptor"
/protein_id="AACS0158.1"
/db_xref="G1:596070"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 439; DB 11;
Pred. No. 4.5e-237;
0; Mismatches 7;
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                                                                                                  1. .1154
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
/map="8q11-12"
                                                                                                                                                                                                  /tissue_type="placenta"
1. .1143
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                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                      /gene="hKOR"
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/qene="hKOR"
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ilarity 99.1%;
Conservative
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      TITLE
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Submitted (03-NoV-1994) David K. Grandy, Vollum Institute, Oregon
Health Sciences Univeristy, 3181 S.W. Sam Jackson Park Road,
Portland, OR 97201, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grandy, D.K.
Mapping of the human kappa opioid receptor gene to chromosome 8q11.2q12: no evidence for multiple kappa opioid receptor genes Unpublished
2 (bases 1 to 1229)
Grandy, D.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   644 CAACCTGCGTAGGATCACCAGACTGGTCCTGGTGGTGGCAGTCTTCGTCGTCTTGCTG 703
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1229)
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                                                             28211: contig of 11952 bp in length gap of unknown length say of unknown length say of unknown length gap of unknown length gap of unknown length contig of 28136 bp in length 108022: contig of 28136 bp in length gap of unknown length gap of unknown length la3066: contig of 3044 bp in length gap of unknown length length
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54893 t 42 others
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             unknown J
of 5582 h
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. 183559
7. organism="Romo sapiens"
Ab_xref="taxon:9606"
/chromosome="11"
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/clone_lib="RPCI-11
/ 36408 c 35313 g
             gap of
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U16860
U16860.1 GI:595932
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Best Local Similarity 100.0
Matches 252; Conservative
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC009646 183559 bp DNA HIG 20-0CT-1999
Homo sapiens chromosome 11 clone 162_D_09 map 11, *** SEQUENCING IN
PROGRESS ***, 10 unordered pieces.
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                                TCTTCACCTTGACCATGATGAGGGTGGACCGCTACATTGCCGTGTGCCGTGTGCCGTGAAGG 339
                                                                                                                                                                                                                                                                                                                                                                            CITIGGACTICCGCACACCCTIGAAGGCAAAGAICATCAAIATCTGCATCTGGCTGCTGT 399
   CTTIAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTGATGAATTCCTGGCCTT 219
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1 (bases 1 to 183559)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 11, clone 162_D_09
Unpublished
                                                                                                                        TIGGGGATGIGCTGTGCAAGATAGTAATTTCCATTGATTACTACAACATGTTCACCAGCA
                                                                                                                                                                                                                                                                                                           TCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTGTGCCACCCCGTGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                    510 CTTTGGACTTCCGCACACCCTTGAAGGCAAAGATCATCAATATCTGCATCTGGCTGCTGT
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* NOIE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGTCATCTGTTGGCATCTCTGCAATAGTCCTTGGAGGCACCAAAGICAGGGAAG
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gap of unknown length
contig of 4054 bp in length
gap of unknown length
contig of 4780 bp in length
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240. 1382
/codon_start=1
/codon_start=1
/inction="G protein-coupled seven-helix receptor,
high-affinity to dynorphin A"
/product="kappa opioid receptor"
/protein_id="AaA67171.1"
/db_xref="G1:476107"
/translation="MGRRRQGPAQPASELPARNACLLPNGSAWLPGWAEPDGNGSAGP
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Zina Pitcher Place, Ann
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Primary structure and functional expression of a guinea pig kappa opioid (dnorphin) receptor

Proc. Natl. Acad. Sci. U.S.A. 91 (9), 3779-3783 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CPU04092 1733 bp mRNA ROD 24-MAY-1995
Cavia porcellus Hartley kappa opioid receptor mRNA, complete cds.
004092
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                                                                                                                                                                                                                                                                                                                                            70 GCCGIGIGCCACCCCGIGAAGGCITIGGACTICCGCACACCCTIGAAGGCAAAGAICAIC 129
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                                                                                                                                                                                                                                                                                                          318 GCCGIGIGCCACCCCGIGAAGGCTTIGGACTTCCGCACACCCTIGAAGGCAAAGAICAIC 377
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Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
1 (bases 1 to 1733)
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Submitted (07-DEC-1993) Guo-xi Xie, Mental )
Institute, The University of Michigan, 205
Arbor, MI 48109-0720, USA
Location/Qualifiers
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                                                                                                                                                            tch 19.6%; Score 196; DB 9; 3 sal Similarity 100.0%; Pred. No. 1.3e-99; 196; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Cavia porcellus"
/strain="Hartley"
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/protein_id="AAA63646.1"
/db_xref="GI:598185"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="brain"
/dev_stage="adult"
1. .239
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/clone_lib="pME18S"
/sex="male"
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Cavia porcellus
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                                                                                                                                                                                                                                                                                                                                                                                                      /translation="KIVISIDYYNMFTSIFTLTMMSVDRYIAVCHPVKALDFRTPLKA
                                                                                                                                                                                                                                                                          /note="encodes putative transmembrane domains III and IV, smillar to mouse kappa type opioid receptor, SwissProt Accession Number P33534" /codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang, W. J. Johnson, P.S., Wu, J.M., Wang, W.F. and Uhl, G.R. Human kappa opiate receptor second extracellular loop elevates dynorphin's affinity for human mu/kappa chimeras J. Biol. Chem. 269 (42), 25966-25969 (1994)
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Homo sapiens kappa opiate receptor mRNA, partial cds.
L36130
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 432)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          22 others
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/product="kappa opiate receptor"
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/db_xref="G1:595933"
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/db_xref="taxon:9606"
                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
   Location/Qualifiers
1. .1229
                                                                                              /sex="male"
/dev_stage="adult"
/map="8q11.2-q12"
/chromosome="8"
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kappa opiate receptor.
Homo sapiens cDNA to mRNA.
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                                                                                                                                                                                                      1. .219
/gene="OPRK1"
                                                                                                                                                                                                                                                          /gene="OPRK1"
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/product="kappa opioid receptor"
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/d_xref="c1:4102308"
/d_xref="c1:4102308"
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FRTPLKAKIINICIWILSSSVGISAIVLGGTKVREDVDVIECSLQFPDDDYSWWDLEV
FRTPLKAKIINICIWILSSSVGISAIVLGGTKVREDVDVIECSLQFPDDDYSWWDLEV
VCWTPHIFILIVAGALGSTRHWALLSRYSVFCIALGYTNSSLNPILYAFLDENFRRGFR
DFGFPVKVRMERQSTSRIKN"
a 225 c 175 g 176 t
QDBQLEPAHISPAIPVIITAVYSVVFVVGLVGNSLVMFVIIRYTKMKTATNIYIFNLA
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CHPVKALDFRYPLKAKIINICHWLLSSSVGISBAILIGGTKVEBDVDIIECSLQFPDDD
YSWWDLFMKICVFVFAFFYDYLIITVYTLMILRLKSVFLLSGSREKDRNLRFITRLY
LVVVARTICWFPIFFILYEBLGGSFGSFGSFGSTSSYFFCIALGYTNSENPILYAFLD
ENFKRCFRDFCFPIKMEMERQSTSRVRNIVQDPAYMRNVDGVNKFV"
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Pampusch,M.S.
Direct Submission
Submitted (01-JUL-1997) Veterinary Pathobiology, University of
Minnesota, 1971 Commonwealth Ave, 205 Veterinary Science, St. Paul,
MN 55108, USA
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                                                                                                                                                                                                                                  Gaps
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Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (Dases I to 715)
Pampusch, M.S., Zilliox, M., Osinski, M.A., Brown, D.R. and Murtaugh, M.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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2.6e-15;
hes 0;
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/tissue_type="cerebral cortex"
<1..>715
                                                                                                                                                                                      4.7%; Scor.
100.0%; Pred. No. 2...
... 0; Mismatches
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                                                                                                                                    403
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/evidenceexperimental
/product="Rappa opioid receptor"
/product="Rappa opioid receptor"
/b_xref="G1:595575".
/db_xref="G1:595575".
/translation="YTKMRTAINIYIENLILADALVTINPFOSAVYLMNSWPFGDVL
CKIVISIGGTNWFTSIFTLIMMSVDRYIAVCHPVKALDFRTPLKAKIINICIWILASS
VGISALUGGTKWAF 35 g 141 t
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                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (07-Nov-1994) David K. Grandy, Vollum Institute, Oregon Health Sciences, University, 3181 S.W. Sam Jackson Park Road, Portland, OR 97201, USA Location/Qualifiers
                                                                                                                                                                                                                                            Mapping of the human kappa opicid receptor gene to chromosome 8q11.2-q12: no evidence for multiple kappa opicid receptor genes Unpublished
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Nishi,M., Takeshima,H., Mori,M., Nakagawara,K. and Takeuchi,I.
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                07-DEC-1994
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                                   partial cds.
                                                                                                                                                                            Mammalia;
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 432)
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Mus musculus
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MMU16998 432 bp DNA
Mus musculus kappa opioid receptor (oprkl)
U16998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Stratagene lambda FIX" /sex="male"
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100.0%; Pred. No. 2e-
ilve 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="R21mg1"
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14. .366
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/note="encodes
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14. .366
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                                                                                U16998.1 GI:595936
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                                                                                                                               mouse.
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1 (bases 1 to 1408)
Kieffer, B.L., Matthes, H.W., Simonin, F.H., Dierich, A. and Lemeur, M.
IRANGCENIC ANIMAL WHOSE EXPRESSION OF THE OPIATE RECEPTORS IS
MODIFIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu, H.C., Lu, S., Augustin, L.B., Felsheim, R.F., Chen, H.C., Loh, H.H. and Wei, L.N.
and Wei, L.N.
Cloning and promoter mapping of mouse kappa opioid receptor gene Biochem. Biophys. Res. Commun. 209 (2), 639-647 (1995)
                                                                                                                                                                                                                                                                                                                                                                         87786882 1109 bp DNA ROD 26-SEP-1995
Rappa opioid receptor [mice, Genomic, 1109 nt, segment 2 of 5].
877869.1 GI:998530
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1109)
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3.3%; Score 33; DB 12; I
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 33; Conservative 0; Mismatches 0;
                                       /evidence=experimental
/product="kappa opioid receptor"
579. .>658
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                                                                                                                                                                                                   Query Match 3.3%; Score 33; DB Best Local Similarity 100.0%; Pred. No. 2.1 Matches 33; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                               548 ATAGTCCTTGGAGGCACCAAAGTCAGGGAAGGT 580
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Sequence 5 from Patent W09802534.
A68828
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213 c 204 g
                                                                                                               /evidence=experimental
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                                                                                                                            Submitted (28-MAY-1994) to the DDBJ/EMBL/GenBank databases. Hiroshi Takeshima, Tokyo Institute of Psychiatry, Department of Neurochemistry; 2-1-8 Kamikitazawa, Setagaya-ku, Tokyo 156, Japan (Tel.03-3304-5701(ex.312), Fax:03-3829-8035) Submitted (28-May-1994) to DDBJ by:
Hiroshi Takeshima
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Structure and chromosomal mapping of genes for the mouse kappa-opioid receptor and an opioid receptor homologue (MOR-C) Biochem. Biophys. Res. Commun. 205 (2), 1353-1357 (1994) 95100967
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1 (bases 1 to 658)
Yakovlev,A.G., Krueger,K.E. and Faden,A.I.
Structure and expression of a rat kappa opioid receptor gene 95204422
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Rattus norvegicus kappa opioid receptor gene, exon 3.
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/db_xref="taxon:10116"
/sex="male"
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                                                                                                                                                                                                                                     Department of Neurochemistry
Tokyo Institute of Psychiatry
2-1-8 Kamikitazawa, Setagaya-ku
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Phone: 03-3304-5701 x312
Fax: 03-3329-8035.
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Takeshima, H.
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Yakovlev, A.G.
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Other publication FR 2750825 19980116.
Location/Qualifiers
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Search completed: February 17, 2000, 10:10:57 Job time: 1972 sec

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Copyright (c) 1993 - 1998 Compugen
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US-08-417-103-5
US-08-417-103-5
US-08-417-103-15
US-08-468-036-43
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Sequence 11, Appl
Sequence 15, Appl
Sequence 43, Appl
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APPLICANT: EVANS, CHRISTOPHER J.
APPLICANT: EDWARDS, ROBERT H.
TILLE OF INVENTION: RECEPTOR, RELATED EXPRESSION SYSTEMS, TILLE OF INVENTION: PHARMACEUTICALS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE SIDERSS:
ADDRESSEE: Mortison & Foerster
STREET: 775 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1829;
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/411,859
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100.0%; Pred. No. 2.5e-05;
tive 0; Mismatches 0;
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FILING CANADATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
CLING DATE: 13-AUG-1992
ATIORNEY/AGENT INFORMATION:
NAME: LITHGOW, IIMOHIY J.
REGISTRALION NUMBER: 36,856
REFERENCE/DOCKET NUMBER: 22000-20526.00
TELECOMMUNICATION INFORMATION:
IELEPHONE: 415-494-0792
                                                                                                                                                                                                                                                                                               US-08-411-859-1; Sequence 1, Application US/08411859; Patent No. 5985600
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PC-DOS/MS-
SOFTWARE: PatentIn Release #
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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California
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NAME: WILSON, MARK B. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY:
; LOCATION:
PCT-US94-10358-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
PCI-US94-10358-7
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏΔ
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0
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PCT-US94-10358-1
| Sequence 1, Application PC/TUS9410358
| Sequence 1, Application PC/TUS9410358
| Sequence 1, Application PC/TUS9410358
| TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS |
| TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS |
| TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS |
| TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS |
| TITLE OF INVENTION: Multe & Durkee |
| TITLE OF INVENTION: Multe & Durkee |
| TITLE OF INVENTION: Multe & Durkee |
| TITLE OF INVENTION: MULTER ADDRESSE: ADDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.6%; Score 26; DB 6; Length 1618; Best Local Similarity 100.0%; Pred. No. 0.00076; Matches 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER ENDABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPAGE
COMPUTER: IBM PC COMPAGE
SOFTWARING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARING PATENTIN NELEASE #1.0, VERSION #1.25
CURRENT APPLICATION NERE: PCT/US94/10358
FILING DATE: COMCURTENTLY herewith
PRIOR APPLICATION NUMBER: 08/120.601
PFILING DATE: 13 SEPTEMBER 1993
ATPORNEY/AGENT INFORMATION:
NAME: WILLSON, MARK B.
REGISTRATION NUMBER: 37,259
REBEBROCE/POCKET NUMBER: 37,259
REBEBROCE/POCKET NUMBER: 37,259
REBEBROCE/POCKET NUMBER: 1000
TELEPAN: (713) 789-2679
291 ACCATGATGAGCGTGGACCGCTACATTGC 319
                                                   446 ACCAIGATGAGGGGGGGCCTACATTGC 474
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214..1410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) NAME/KEY:
) LOCATION:
PCT-US94-10358-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
PCT-US94-10358-3
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Gaps
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TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDIA, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STREET: Texas
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
2.6%; Score 26; DB 6; Length 1618;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPOTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIDLE
COMPATION SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358
FILLING DATE: CONCURTENTLY herewith
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
13 SEPPEMBER 1993
ATORNEY/AGENT INFORMATION:
NAME: WILSON, MARK 37, 259
RESISTRATION NUMBER: 37, 259
REFERENCE/DOCKET NUMBER: INDA005P--
TELECHONE: (512) 418-3000
TELECHONE: (512) 418-3000
TELECHONE: (512) 789-2679
                                                                                                                                                                           APPLICATION NUMBER: PCT/US94/10358 FILING DATE: Concurrently herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255 GATTACTACAACATGTTCACCAGCAT 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    652 GATTACTACAACATGTTCACCAGCAT 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application PC/TUS9410358 GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/120.601
FILING DATE: 13 SEPTEMBER 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (713) 789-2679
TELEF : 79-0924
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37,259
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339..1235
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linear
                                                                                                                                                                                                                                                                                                                                            Texas
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US-07-816-283-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-149-093A-3
                                                                US-07-816-283-3
                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
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                                                                                                                                                                                                                                                                                                                     Length 1610;
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                                                                                                                                                                                                                                                                                                                Query Match 2.5%; Score 25; DB 6; Length 161
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLY:...
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTRY: USA
ZIP: 77210
COMPUTRY: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/816,283
FILING DATE: 19911231
CLASSIFICATION: 435
ATIORNEY/AGENT INFORMATION:
NAME: MCDAniel, C. Steven
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-815-283-1

Sequence 1, Application US/07816283

Patent No. 5486155;
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I.
APPLICANT: Yamada, Yuichiro
APPLICANT: Yamada, Yuichiro
APPLICANT: Selno, Susumu
ITLE OF INVENTION: SOMATOSTATIN RECEPTORS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSES: Arnold, White & Durkee
STREET: PO Box 4433

CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
REFERENCE/DOCKET NUMBER: INDA005P-TELECOMMUNICATION INFORMATION:
FELENCHONE: (512) 418-3000
FELENCEAX: (713) 789-2679
FELEX: 79-0924
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
FENTH: 1610 base pairs
FYPE: nucleic acid
STRANDEDNESS: single
FOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                        1113 rcgrcrgcrggacrcccarrcacar 1137
                                                                                                                                                                                                                                                                                                                                                                                                  694 TCGTCTGCTGGACTCCCATTCACAT 718
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Best Local Similarity 100.0%; P. P. Consorvative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 713-789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263 CAACAIGTICACCAGCAICT 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: NUCLEIC ACID-
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: lin
; MOLECULE TYPE:
US-07-816-283-1
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APPLICANT: Bunzow, James R
APPLICANT: Bunzow, James R
APPLICANT: Grandy, David K
TITLE OF INVENTION: A No. 5558783el Mammalian Methadone-Specific
TITLE OF INVENTION: Opioid Receptor Gene and Uses
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
STREET: Illnois
COUNTRY: USA
ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                       COUNTY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OFFRAING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/816,283
FILING DATE: 19911231
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
0.72;
                                            GENERAL INFORMATION:
APPLICANT: Bell, Graeme I.
APPLICANT: Yamada, Yuichiro
APPLICANT: Seino, Susumu
APPLICANT: Seino, Susumu
TITLE OF INFORTION: SOMATOSTATIN RECEPTORS
VUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 20; DB 1; Pred. No. 0.72 0; Mismatches
                                                                                                                                                                                              ADDRESSEE: Arnold, White & Durkee STREET: PO Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08149093A; Patent No. 5658783
Sequence 3, Application US/07816283
Patent No. 5436155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pow Matches 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 60606
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEPRAX: 713-789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 CAACATGITCACCAGCAICI 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              504 CAACATGITCACCAGCATCT 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1265 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IELERAX: 713-789-2679
IELEX: 79-0924
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1265 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: NUCLEIC ACID-
STRANDEDNESS: double
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                 Length 1634;
                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SITELL FOUR 44433
SITELL FOR 44433
SITEL TEXAS
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: TEM PC COMPATIBLE
COMPUTER: PATENTIA RELEASE #1.0, Version #1.30
SOFTWARE: PATENTIA RELEASE #1.0, Version #1.30
SOFTWARE: O5-APR-1995
CLASSIFICATION NUMBER: US/08/417,103
FILING DATE: 05-APR-1995
CLASSIFICATION NUMBER: US 07/816,283
FILING DATE: 01-DEC-1991
ATTOMENYAGENT IRFORMATION:
ATTING DATE: 01-DEC-1991
ATTOMENYAGENT IRFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.0%; Score 20; DB 2; Best Local Similarity 100.0%; Pred. No. 0.73; Matches 20; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Bell, Graeme I.
APPLICANT: Yamada, Yuichiro
APPLICANT: Seino, Susumu
TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSES:
ADDRESSES:
ADDRESSES:
ADDRESSES:
CITY: Houston
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:144
TELECOMMINICATION INFORMATION:
TELEFONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISICS:
LENGTH: 1634 base pairs
TYPE: nucleic acid
SIRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RECISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 474-757
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1265 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-08-417-103-3
Sequence 3, Application US/08417103
; Patent No. 5723299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       516 CARCATGTTCACCAGCATCT 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 CAACAIGTICACCAGCATCT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Wilson, Mark B. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                   CDS
100..1272
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88..1260
                                                                                                                                                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-08-417-103-1
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US-08-417-103-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/417,103 FILING DATE: 05-APR.1995 CLASSIFICATION: 435
        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENI APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08417-103-1
Sequence 1, Application US/08417103
Patent No. 5722299
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I.
APPLICANT: Yamada, Yuichiro
APPLICANT: Seino, Susumu
ITILE OF INVENTION: SOMATOSTATIN RECEPTORS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                              CORRENT AFFLICATION DAYS

PULING DAYE: 05-008/149,093A

CLASSIFICATION 1435

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 35,003

REFERENCE/DOCKET NUMBER: 93,311

TELECOMMUNICATION INFORMATION:

TELEFRAE: 312-715-1234

INFORMATION FOR SEQ ID NO: 3:

SEGUENCE CHARACTERISTICS:

LENCTH: 1452 base pairs
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APPLICATION NUMBER: US 07/816,283
FILLING DATE: 01-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Texas
COUNIRY: United States of America
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: RC-DOS/NS-DOS
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1283..1452
                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
182..1282
                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5'UTR
1..181
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
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Sequence 3, Application US/08911245

Patent No. 5821067

GENERAL INFORMATION:
APPLICANT: Bunzow, James R
APPLICANT: Grandy, David K
ITILE OF INVENTION: A No. 5811067el Mammalian Methadone-Specific TITLE OF ENVENTION: Opioid Receptor Gene and Uses
CORRESPONDENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                   TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: KAPPA3 OPIOID RECEPTORS, RECEPTOR.
TITLE OF INVENTION: ENCODED THEREBY, AND USES THEREOF
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
0.74;
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STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: 111inois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.0%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 0.7 Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                              COUNTY 10036
COMPUTER RELDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.30
SOFTWARE: Patentin Release #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,949A
FILING DATE: OS-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORM
                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
CITY: New York
STAIE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2600 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
Pan, Ying-Xian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: 299..14
; OTHER INFORMATION:
US-08-147-949A-1
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                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                             STATE: No COUNTRY:
APPLICANT:
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                                                                                          Gaps
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                      Length 1265;
                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,103
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
                   Query Match 2.0%; Score 20; DB 2; Best Local Similarity 160.0%; Pred. No. 0.72; Matches 20; Conservative 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOMATOSTATIN RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 05-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION NUMBER: US 07/816,283
FILING DATE: 01-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: WISON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKEI NUMBER: ARCD:144
TELEPHONE: (512) 414-3600
TELEPHONE: (512) 414-3507
INFORMATION POR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bell, Graeme I.
APPLICANT: Bell, Graeme I.
APPLICANT: Selno, Yuichiro
APPLICANT: Selno, Susumu
TITLE OF INVENTION: SOMATOSTATIN RECE.
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
SIREEI: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States of America
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US-08-147-949A-1
; Sequence 1, Application US/08147949A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 13, Application US/08417103
; Patent No. 5723299
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 CAACATGTTCACCAGCATCT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 431 CAACATGITCACCAGCATCT 450
                                                                                                                                                  263 CAACATGTTCACCAGCATCT 282
                                                                                                                                                                                                               504 CAACATGTTCACCAGCAICT 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1205 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
15..1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid<sup>*</sup>
STRANDEDNESS: sing<sup>†</sup>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: UR
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US-08-417-103-13
                                                                                                                                                                                                                                                                                                                                       US-08-417-103-13
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Gaps

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Length 2600;

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Query Match 2.0%; Score 20; DB 2; Length 1452; Best Local Similarity 100.0%; Pred. No. 0.72; Matches 20; Conservative 0; Mismatches 0; Indels
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Patent No. 5837809

GENERAL INFORMATION:
APPLICANT: Bunzow, James R.
APPLICANT: Grandy, David K.
APPLICANT: Grandy, David K.
APPLICANT: Reinscheid, Rainer K.
APPLICANT: Monsma, Frederick J.
TILLE OF INVENTION: A NOVEL MAMMALIAN OPICID
TITLE OF INVENTION: RESPECT LIGAND AND USES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                 REFERENCE/DOCKET NUMBER: 899-40006/WDN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSE: Klarquist Sparkman Campbell ADDRESSE: Leigh & Whinston LLP STREET: 121 S.W. Salmon, Suite 1600 CITY: Portland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 08/11/95
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/553,058
FILING DATE: 11/13/95
ATTORNEY CAPATE: 11/13/95
ATTORNEY CAPATE: NILITAM D. NO. 5837809nan, M.D.
                       ATTORNEY/AGENT INFORMATION:
NAME: William D. No. 5821219nan, M.D.
REGISTRATION NUMBER: 30,878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WP5.1 ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/514,451A
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1283..1452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
182..1282
                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
DESCRIPTION: CDNA
FEATURE:
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1..181
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Y: USA
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FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) NAME/KEY:
) LOCATION:
US-08-553-058C-3
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US-08-514-451A-3
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Patent No. 5821219
GENERAL INFORMATION:
APPLICANT: Grisel, Judith E.
APPLICANT: Mogil, Jeffrey S.
TITLE OF INVENTION: Opioid Antagonists and Methods of Their Use NUMBER OF SEQUENCE: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Klarquist Sparkman Campbell Leigh & Whinston LLP STREET: 121 S.W. Salmon, Suite 1600 CITY: Portland STATE: Oregon COUNTRY: USA
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        OPERATING SISIEM:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,245
FILING DATE: 15-40G-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149093
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/149093
FILING APPLICATION NUMBER: 93,311
FILING DATE: 06-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5821067nan, Kevin E
REGISTRATION NUMBER: 93,311
TELEFRAK: 312-715-100
TELEFRAK: 312-715-100
TELEFRAK: 312-715-103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.0%; Score 20; DB 2; Best Local Similarity 100.0%; Pred. No. 0.72; Matches 20; Conservative 0; Mismatches (
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MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFIWARE: Version WF6, ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,058C
FILING DATE: 11/3/95
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
OPERATING SYSTEM: PC-DOS/MS-DOS
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FEATURE:
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US-08-911-245-3
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US-08-553-058C-3
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FEATURE:
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2.0%; Score 20; DB 3; Length 2706; ilarity 100.0%; Pred. No. 0.74; Conservative 0; Mismatches 0; Indels
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                                              TOPOLOGY: linear
MOLECULE IYPE: CDNA
ORIGINAL SOURCE:
TISSUE IYPE: Rat brain
US-08-454-549-1
               STRANDEDNESS: single
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Best Local Similarity
Matches 20; Conserva
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| Patent No. 586534
| GENERAL INFORMATION
| APPLICANT: EPPLER, C. Mark
| APPLICANT: OZENBERGER, Bradley A. APPLICANT: OZENBERGER, Bradley D. APPLICANT: HULMES, Jeffrey D. TITLE OF INVENTION: TO OPIOID RECEPTORS
| VUMBER OF SEQUENCES: 13
| CORRESPONDENCES: 13
| CORRESPONDENC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,549
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGRNY INFORMATION:
NAME: Robinson, Joseph R.
REGISCHATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/IA818-US5
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 527-7700
TELEFAX: (212) 527-7700
TELEFAX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRARCIBELSTICS:
LENGTH: 2706 base pairs
TYPE: nucleic acid
REGISTRATION NUMBER: 30,878

REFERENCE/CDCKET NUMBER: 899-45995/WDN
TELECOMMUNICATION INFORMATION:
TELEPRAX: (503) 228-7391
TELEPRAX: (503) 228-7446
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 base pairs
TYPE: UNCALSIC acid
STRANDEDNESS: single
TOPOLOGY: linear
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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1283..1452
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182..1282
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MOLECULE TYPE:
DESCRIPTION: CDNA
FEMIURE:
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LOCATION:
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NAME/KEY:
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US-08-514-451A-3
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US-08-454-549-1
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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gb_gss10:*
gb_gss11:*
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gb_gss12:*
gb_gss13:*
## Comparison of the compariso
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gb_gss15:*
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                 GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.
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                                                                                                                                                                                                          Title:
Perfect
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R31994 Yh62c10.r1 R81583 Yj04b04.r1 A1980732 pat.pk003 M75869 CEL06A11 Ch D75109 CELK096D7F AA317847 EST19840 AA447244 zw93c04.r

R31984 R81583 A1980732 M75869 D75109 AA317847

2220222 2220322 344032

Description

SUMMARIES

This clone is available royalty-free through LINE; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 947 Std Error: 0.00 Seq primer: MASH: 947 Std Error: 0.00 Seq primer: MASH: 120.  High quality sequence stop: 120.  Location(Qualitiers)  / GL Xref="amon sapiens"   Acquains   A	RESULT 2 R81583 LOCUS YO 4004.r1 Soares placenta ND2HP Homo sapiens CDNA clone IMAGE:147727 5' similar to q9:L25119 MJ-TYPE OPTOID RECEPTOR ACCESSION VERSION R81583.1 GI:858186 RST. R91583.1 GI:858186 RST. ROCCESSION VERSION R91583.1 GI:858186 RST. ROCCESSION R91583.1 GI:858186 RST. REFERENCE HIller,L., Clark,N., Dubuque,T., Flliston,K., Hawkins,M., HILLER, M., HILLMAN,M., Kucaba,T., Le,M., Lennon,G., Marra,M., HILLER, M., HILLMAN,M., RUCAba,T., Soares,M., TTEVASKIS,E., Waterston,R., Williamson,A., Wohldmann,P. and TITLE The Washl-Marck EST Project JOURNAL ON MAY 8. 1995 this sequence version replaced gi:800395. Contact: Wilson RK Washington University School of Medicine 4444 Forest Parkway, Box 8501, St. Louis, MO 63108 FAX: 314 286 180 F
AISS4367 Oy48c06.x AISS4239 thildil.x AISS4367 tnclbil2.x AV192296 AV192296 AV9192296 AV192296 AV312772 AV31272 AV3172 AV3172 AV3172 AV3172 AV3172 AV3172 AV3172 AV3172 AV3172 AV3173 AV317	EST 28-APR-1995 sapiens CDNA clone fu-TYPE OPIOID RECEPTOR  U, Vertebrata; Mammalia; dae; Homo. s.ton,K., Hawkins,M., Aston,K., Tan,F., Aston,M.,
19 1.9 443 41 AIOSG367 19 1.9 523 48 AIS53367 19 1.9 523 48 AIS53367 19 1.9 578 63 AIS53267 19 1.9 578 63 AV92296 11.9 161 71 AV312772 11.9 683 AV950015 11.9 523 63 ANV183364 11.9 525 74 AW183364 11.9 525 74 AW183364 11.9 525 74 AW18364 11.9 525 74 AW180366 11.9 525 74 AW180366 11.9 525 74 AW180366 11.9 525 74 AW180366 11.9 525 100 AQ237774 11.9 528 100 AQ237767 11.9 528 100 AQ237766 11.8 524 105 AQ20195 11.8 524 105 AQ201166 11.8 525 100 AQ237167 11.8 525 AV31167 11.8 532 25 N97151 11.8 532 25 N97151 11.8 532 25 N976111 11.8 532 25 N976111 11.8 532 33 AA31167 11.8 532 33 AA31209 11.8 532 38 AA749488	ALIGNMENTS  R31984 153 bp mRNA EST 28-APR-1995 yh62c10.r1 Scares placenta ND2HP Homo sapiens CDNA clone IMAGE:134322 5' similar to qb:L25119 MU-TYPE OPIOID RECEPTOR R31984.1 G1:787827 R31984.1 G1:787827 human. Homo sapiens EVARATYOTA; METAZOA; Chordata; Craniata; Vertebrata; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 153) H111ler.L., Clark, M., bubuque, T., Elliston, K., Hawkins, M., H111ler.L., Clark, M., bubuque, T., Elliston, K., Hawkins, M., H111ler.L., Hilfman, M., Kucaba, T., Le, M., Lennon, G.; Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Scares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. The Washu-Merck EST Project Unpublished (1995) Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Fax: 314 286 1800

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

RESULT 1 R31984 LOCUS DEFINITION

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/lab_host="E.coli IOP10 F'"
                    r: pcDNA3"
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                                                                                2.0%; SCOL.
100.0%; Pre
0;
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                 /note="Vector:
130 c 16
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Caenorhabditis elegans
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                                                                                                           Similarity
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                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                              DEFINITION
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JOURNAL
MEDLINE
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Ass; Neodanthae; Galliformes; Phasianidae; Phasianinae; Gallus. 1 (Dases 1 to 659)
Tirunagaru, V.G., Sofer, L. and Burnside, J.
An expressed-sequence-tag database of activated chicken T cells: Sequence analysis of 5596 clones
Unpublished (1999)
On Dec 20, 1995 this sequence version replaced gi:1130941.
Contact: Joan Burnside
Molecular Endocrinology
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considerated overall poor quality Insert Length: 1518 Std Error: 0.00 Seq primer: M13RPl High quality sequence stop: 1. Localion/Qualifiers 1.183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:903".
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/clone="pat.pk0032.bl2.f"
/clone_lib="chicken activated T cell cDNA"
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/sex="Female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Gallus gallus"
                                                                                                                      /organism="Homo sapiens"
/db_xref="GDB:559413"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          644 CAACCIGCGIAGGAICACCAGACIGGICCIGGI
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Location/Qualifiers
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Fax: 302 831-3651
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A1980732
A1980732.1 GI:5883760
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Contact: Waterston R.H.(USA) and Sulston J.E.(UK)
(USA) Dept. of Genetics or (UK)
(USA) Washington Univ. School of Medicine or (UK) MRC Laboratory of
Molecular Biology
Box 8232,4566 Scott Ave., St. Louis, MI 63110, USA, or, Hills
Road Cambridge CB2 20H, UK
Tel: (USA) (314)3627072 or (UK) (0223)248011
Fax: (USA) (314)3624137 or (UK) (0223)42008
Email: rw@nematode.wustl.edu or jes@mrc-lmba.cambridge.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hermaphrodite cDNA library. Partially normalized by successively picking groups of clones that didn't hybridize to previously picked clones. Vector: lambdaphage SHIX2 (lipshitz, D.H. et al., Gene 88:25-36 (1990)) Host: MC1061"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota: Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditodea; Rhabditidae; Peloderinae; Caenorhabditis. 1 (bases 1 to 415).
Harina: Loubin, R., Martin, C., Craxton, M., Huynh, C., Coulson, R., Hillier, L., Durbin, R.K., Green, P., Shownkeen, R., Halloran, N., and Sulston, J., Wilson, R., Berks, M., Du, Z., Ihomas, K., Thierry-Mieg, J. and Sulston, J.
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12
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/strain="Bristol N2"
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11;
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100.0%; Pred. No. 37;
iive 0; Mismatches
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137
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Pred. No.
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Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., '
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M., and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
On Sep 12, 1996 this sequence version replaced gi:1402207.
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699423
Email: arkerlav@tigr.org
Froz clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.html)
Seq primer: Mi3 Reverse.
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1 (bases 1 to 521)

2 (bases 1 to 521)

3 (bases 1 to 521)

3 (bases 1 to 521)

4 (bases 1 to 521)

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6 (bases 1 to 521
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult"
/note="Organ: retina; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 206;
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100.0%; Pred. No. 37;
ive 0; Mismatches 0;
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/db_xxef="taxon:9606"
/clone_lib="Retina II"
/sex="mixed"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA447244.1 GI:2159909
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S Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gooane, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geophagen, N.S.,
Glodek, A., Gnehm, C.L., Hanne, M.C., Hankle, P.S. Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Sprige, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hadson, P.S., Olsen, H.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
                                                                                                                                                                                                                                              Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditina; Rhabditina; Rhabditina; Rhabditina; Rhabditina; Rhabditina; Rhabditina; Rhabditina; Rhabditis.
I (bases 1 to 360)
Kohara,Y., Mitsuki,H., Nishigaki,A., Motohashi,T., Sugimoto,A. and
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                               D75109 360 bp mRNA EST 18-OCT-1999 CELK096D7F Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk96d7 5', mRNA sequence.
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Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/strain="N2"
/db_xref="taxon:5239"
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hermaphrodite embryo"
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/dev_tarage="embryo"
/ dev_tarage="embryo"
/ dev_tarage="embryo"
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EST19840 Retina II Homo sapiens cDNA 5' end, mRNA sequence.
AA317847 GI:1970173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1994)
Contact: Yuji Kohara
Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Ta: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp
High quality sequence stop: 322.
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1. .360
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tive 0;
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement. Ash Alizadeh, John Byrd, M.D., Mike Grever,
Tissue Procurement. M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCL-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
AIS24239 523 bp mRNA EST 18-MAR-1999 th11d11.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2117973 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Primates: Catarrhini; Hominidae; Homo.

1 (bases 1 to 523)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/clone_1b="NGT_CGAP_CLL1"
/tissue_type="B-cell, chronic lymphotic leukemia"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Inpublished (1997)
On Jul 1997)
Con Jul 1997, this sequence version replaced gi:2285735.
Contact: Robert Strausberg, Ph.D.
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37;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                  1.9%; Score 19;
100.0%; Pred. No.
tive 0; Mismatch
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Location/Qualifiers
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Matches 19; Conserv
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NOLYMINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/PHGAP), Tumor Gene Index

(CGAP/PHGAP), Tumor Gene Index

L Unpublished (1998)

On Sep 12, 1996 this sequence version replaced gi:1404573.

Contact: Robert Strausbergenih.gov

Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                    CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI056367 443 bp mRNA EST 24-SEP-1998 oy48c06.xl NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1669066 3',
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Bonaldo, Ph.D.
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100.0%; Pred. No. 37;
ive 0; Mismatches 0; Indels
                                                                                              /clone_lib="Scares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="INAGE:1669066"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
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    .521
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    /db_xref="GDB:5982136"

                                                          /db_xref="taxon:9606"
/clone="IMAGE:784518"
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. Condert-Buck, M.D., Ph.D. Condert-Buck, M.D., Ph.D. Condert-Buck, M.D., Ph.D. Condert-Buck, D.D. Conderts Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center found distribution: NCI-CGAP clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AV192296 378 bp mRNA EST 22-JUL-1999
AV192296 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
embryo Caenorhabditis elegans cDNA clone yk603f8 5', mRNA sequence.
AV192296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="InAGE:255999"
/clone="InAGE:255999"
/clone=lib="NGI_GGAP_GBS4"
/tissue_type="poorly differentiated adenocarcinoma with
signet_ring cell features"
/lab_host="hBHD8"
/note="organ: stomach, Vector: pCMV-SPORI6; Site_1: Sall;
Site_2: Not1: Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"
207 c 207 g 163 t
                                                                                                                AI679822 679 bp mRNA EST 26-MAY-1999 tu66b12.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2255999 3' similar to TR:000112 O00112 LIVER-SPECIFIC BHLH-ZIP TRANSCRIPTION
                                                                                                                                                                                                                                                                                                  Homo Sapiens

Bukaryota, Metazoa: Chordata, Craniata; Vertebrata; Mammalia;
Butheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 679)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
On Dec 20, 1995 this sequence version replaced gi:1131236.
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.9%; Score 19; DB 5
100.0%; Pred. No. 37;
ative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 397.
Location/Qualifiers
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                                                                                                                                                                                    FACTOR; mRNA sequence. A1679822 GI:4890004
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128 GGCACCAAAGTCAGGGAAG 146
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AI679822/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 3/1; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library is normalized, and was constructed by Bento Soares and M-Talma Bonando."
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                                                                                                                                                                                                                                                                              AI559367 233 bp mRNA EST 12-MAY-1999 tr21b12.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2168255 3',
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NCI/NINDS-CGF http://www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-CGF http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/PRGAP), Tumor Gene Index
Unpublished (1998)
On Jun 5, 1998 this sequence version replaced gi:3189024.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Pmail: Robert_Strausberg@nih.gov
                                                                    Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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                 1.9%; Score 19; DB 47; Length 523;
100.0%; Pred. No. 37;
ive 0; Mismatches 0; Indels
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Pred. No. 37;
0; Mismatches
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/clone="IMAGE:2168255"
/clone_lib="NCI_CGAP_Brn25"
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/organism="Homo sapiens"
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Seq primer: -400P from Gibco
High quality sequence stop: 224
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100.0%; Pre
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AI559367
AI559367.1 GI:4509572
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                                                                                                                73 GGAAATGCIATTGTTTCTT 91
                                                                                                                                                              74 GGAAATGCIATTGTTTCTT 92
                                         Best Local Similarity 100.
Matches 19; Conservative
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TITLE
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Length 679; 0; Indels

50;

TITLE JOURNAL

COMMENT

FEATURES

REFERENCE AUTHORS

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Eutheria: Redentia: Sciurognath; Muridae; Murinae; Maumalia; Eutheria: Redentia: Sciurognath; Muridae; Murinae; Mus.

Eutheria: Rodentia: Sciurognath; Muridae; Murinae; Mus.

I (basea: Lto. 161)

Excono, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Fukuda, S., Fukunishi, Y., Itoh, W., Izawa, M., Radota, K., Ragawa, I., Kai, C., Kawai, J., Kikuchi, N., Yolawa, M., Radota, K., Kagawa, I., Kai, C., Matul, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matuyama, T., Mitchi, N., Sanco, M., Sato, K., Shibata, K., Shibata, K., Shibata, K., Shibata, Y., Shipata, K., Sancoto, Y., Shitoka, Y., Shipata, Y., Shipata, Y., Shipata, Y., Shipata, Y., Shipata, Y., Shibata, Y., Sh
                                                                                                                                                                                                                       /note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Bco RI; Plasmid DNA from the normalized library NI_CGAP_Kid5 was prepared, and ss circles were made in vitro. Following HAP purification. This DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDS 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo.
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URL:http://genome.rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
Basaki.N., Izawa.M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Hayashizaki,Y.
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh,M., Ritsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
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                                            /db_xxef="taxon:9606"
/clone="lamaGE:2471355"
/clone=lib="NCI_CGAP_Kid12"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_bost="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63; Length 523;
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                                        /organism="Homo sapiens"
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100.0%; Pred. No.
tive 0; Mismatc
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Tel: +81-298-36-9013
Fax: +81-298-36-9098
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On Jun 22, 1998 this sequence version replaced gi:3248182.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert-Strausbergenih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Prrayed by: Greg Leonon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditias; Rhabditina; Rhabditina; Rhabditina; Rhabditina; L. (Dases 1 to 378)

Kohara,Y., Shin-1,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H., Nishigaki,A., Motchash,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A., Mitani,Y., Iida,K., Ussugi,H., Sugimoto,A., Nomoto,H.
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1 (bases 1 to 523)

NCI-GGAP http://www.ncbi.nlm.nih.gov/nciogap.

NAI-OGAP http://www.ncbi.nlm.nih.gov/nciogap.

NAI-OGAP http://www.ncbi.nlm.nih.gov/nciogap.
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On Jun 22, 1998 this sequence version replaced gi:3247111.
Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:6239"
/clone="yk603f8"
/clone=lib="xuji Kohara unpublished cDNA:Strain
hermaphrodite embryo"
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Pred. No. 37;
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National Institute of Genetics
Nat 1111. Mishima, Shizuoka 411,
Tel: 81-55-81-6854
Fax: 81-559-81-6855
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
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65 c 87 g
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Matches

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AUTHORS TITLE REFERENCE

JOURNAL

COMMENT

FEATURES

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Gaps

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us-08-455-683-11.feb17oligo.rst

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/db_xref="taxon:10090"
/clone="58304021"
/clone_lib="RIKEN full-length enriched, adult male thymus"
/sex="male"
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CM4-CT0041-270899-009-a06 CT0041 Homo sapiens CDNA, mRNA sequence.
AW176530
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Okazaki,Y. and Hayashizaki,Y. Automated filtration-based high-throughput plasmid preparation Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninoi,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 683)
HGGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Onpublished (1999)
On May 18, 1998 this sequence version replaced gi:3137999.
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Pred. No. 37;
0; Mismatches 0; Indels
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                                                                                                                                                                      /organism="Mus musculus"/strain="C57BL/6J"
                                                                                                                                                                                                                                                                    /tissue_type="thymus"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 g
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Fax: +55-11-2707001
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome rotject. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtmil2.pl?tl=CM4&t2=CM4-CT0041-270899-009-a06&t3=1999-08-27&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="Adult" http://dev_stage="Adult" ht
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100.0%; Pred. No. 37;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0041"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stringency conditions."
202 c 140 d 1
                                                                                                                                                                                                                                                                                                           Seg primer: puc 18 forward
High quality sequence start: 53
High quality sequence stop: 662.
Location/Qualifiers
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Matches 19; Conserv
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Release 3.1A John F. Collins, Biocomputing Research Unit. nt (c) 1993-1998 University of Edinburgh, U. Distribution rights by Oxford Molecular Ltd Copyright

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

MasPar time 19.73 Seconds 318.037 Million cell updates/sec Thu Feb 17 11:14:53 2000; Run on:

Tabular output not generated.

>US-08-455-683-12 (1-295) from US08455683.pep 2229 1 YTKMKTATNIYIFNLALADA......NTVQDPAYLREIDGMANKPV 295

Title: Description: Perfect Score:

Sequence:

PAM 150 Gap 11 Scoring table:

170751 seqs, 21266608 residues Searched:

Post-processing:

summaries 0.8 4.5 Minimum Match Listing first

Database:

iparti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part11 18:part18 20:part20 23:part20 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 39:part39 31:part31 32:part37 38:part38 39:part39 39:part39 a-genesed35

Variance 153.726; scale 0.219 Mean 33.708; Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Pred. No.	3.49e-193	2.86e-190	2.86e-190	2.86e-190	5.22e-185	5.22e-185	1.24e-184	1.24e-184	5.44e-173	1:16e-127	1.78e-127	1.78e-127	1.78e-127	2.73e-127	2.73e-127	,6.10e-121
			Description	Human kappa opioid re				σť			Rat kappa opiate rece	Human kappa opioid re	Mouse mu opiate recep	Murine mu-subtype opi	Rat mu opiate recepto	Human mu opioid recep	Rat mu opioid recepto	Human mu opiate recep	Rat delta opiate rece
SUMMARIES			TD	R67672	W30297	R88722	W30298	W44939	R67669	R72591	R76783	W30299	W44937	R65188	R76781	R71966	R71964	R76780	R76782
			DB	12	27	17	27	34	13	74	14	27	34	11	14	13	13	14	14
			Match Length DB	295	380	380	427	380	380	380	380	424	398	356	398	400	398	400	372
	æ	Query	Match	7.66	98.3	98.3	98.3	95.8	95.8	92.6	95.8	90.1	68.4	68.3	68.3	68.3	68.2	68.2	65.1
			Score	2223	2192	2192	2192	2136	2136	2132	2132	2008	1524	1522	1522	1522	1520	1520	1452
		Result	No.	1	7	m	4	ហ	9	7	ω	თ	10	11	12	13	14	15	16

.44e-12	1.44e-120	.44e-12	.05e-11	.80e-11	.90e-11	.00e-11	.95e-11	.95e-11	.95e-11	.89e-8	.96e-6	.96e-6	.01e-5	,15e-5	.15e-5	.79e-5	.24e-5	.22e-5	.22e-5	.57e-5	.66e-4	.62e-4	.72e-4	.60e-4	.84e-3	.84e-3	.35e-3	.35e-3
e of murine d	use delta opioid	se delta opiate r	elta opioid	opioid recept	opioid recept	iorph rec	t methadone-specif	at methadone-specif	orphanin FQ rec	pa-3 opioid	somatostatin	atin	Murine somatostatin r	in	uman somatostatin	tuitary som	psilon opioid rece	at RGH G-protein c	t RGHJP G-protein	uman somatostatin r	silon opicid recep	-protein coupled	urine somatostatin	tein coupled re	an qalanin recept	lanin receptor.	galanin recep	t GalR2 receptor
4862	R67670	4493	6650	7196	6767	7663	2658	8054	2521	7429	3925	3926	3926	3926	9726	750	7298	4875	0272	926	7298	1001	3926	001	9507	44	456	013
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### ALIGNMENTS

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N-PSDS (77531).

N-PSDS (77531).

N-PSDS (77531).

N-PSDS (77531).

Polynclectides and peptides derived from opioid receptor polypeptides - for use in therapeutic compositions and in screening assays for useful drug substances.

Claim 12; Page 236-239; 300pp; English.

The partial amino acid sequence of the novel human kappa opioid receptor. The correspoding gene was isolated from a human brain hippocampus cDNA.

The gene is missing the N-terminal sequence. The C-terminal sequence is very similar to the mouse kappa opioid receptor sequence is very similar to the mouse kappa opioid receptor sequence is C-terminal 293 amino acids, 281 residues are identical and 6 residues have conservative substitutions. The gene encoding the human opioid receptor can be placed in a sultable expression vector for production of
                                                                   Human kappa opicid receptor partial protein.
Mouse; kappa; delta; mu; opicid receptor; brain; primer; PCR; amplify;
transmembrane domain; somatostatin; receptor; human; expression vector;
                                                                                                                                                                                /label= Any amino acid
misc_difference 181
                                                                                                                                                                                                                                   label= Any amino acid
                                                                                                                                                                                                                                                                       /label= Any amino acid
                                                                                                                                                                                                                                                                                                          /label= Any amino acid
                                                                                                                                                             Location/Qualifiers
                                                                                                                             truncate; chimaeric; assay; probe.
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WPI; 95-022804/03.
.r
R67672 standard; Protein; 295
R67672;
                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                            20-MAY-1993; US-066296.
30-JUL-1993; US-100694.
05-NOV-1993; US-147592.
(ARCH-) ARCH DEV CORP.
                                                                                                                                                                                                                                                                                                                                            08-DEC-1994.
20-MAY-1994; U05747.
                                                                                                                                                                                                                                                    misc_difference 265
                                                                                                                                                                                                                                                                                        misc_difference 269
                                                                                                                                                                              misc_difference 169
                                                                                                                                              Homo sapiens.
                                                  18-AUG-1995
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the protein in a cell. The opioid receptors thus produced are useful for the development of novel assays designed to select or improve substances, capable of interacting with the opioid receptor proteins, for use in diagnosis, dury design and therapeutic applications.
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                                                                                                                                   FILIMMSVDRYIAVCHPVKALDFRTPLKAKIINICIWLLSSSVGISAIVLGGTKVREDVD 120
                                                                                                                                                       121 viecclqfpdddyswwdlfmkicvfifafvipvliiivcytlmilrlkxvrllsgsrekd 180
                                                                                               ytkmktatniyifnlaladalvtttmpfqstvylmnswpfgdvlckivisidyynmftsi 60
                                                                      Gaps
                                                                                                                                                                                                  181 XNLRRITRLVLVVVAVEVVCWTPIHIFILLVEALGSTSHSTAALSSYYFCIALGYTNSSLN
                                                                                                                        ftltmmsvdryiavchpvkaldfrtplkakiiniciwllsssvgisaivlggtkvregvd
                                                                                                                                                                       121 VIECCLOFPDDDYSWWDLFMKICVFIFAFVIPVLIIIVCYTLMILKLKXVRLLSGSREKD
                                                                                                                                                                                        xnlrritrlvlvvvavfvvcwtpihifilvealgstshstaalssyyfcialgytnssln
                                                                                                                                                                                                                          pilyafldenfkrcfrdfcfplkmxmerxstsrvrntvqdpaylreidgmmnkpv 295
                                                                                                                                                                                                                                    Human kappa opioid receptor.
Selective target cell activation; G protein-coupled receptor;
RASSL; gene therapy; cell prolliferation; kappa opioid receptor;
human; transgentc animal; arrhythmia; bone disease; seizure;
vascular contraction; disease model.
                                                                      ;
                                                     Length 295;
                                                                      1; Indels
                                                    Score 2223; DB 12;
Pred. No. 3.49e-193;
                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "Extracellular"
33.154
Tabel= TMH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74..196
| TMH4
| note= "transmembrane"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "transmembrane"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= TMH5
/note= "transmembrane"
248..275
                                                                                                                                                                                                                                                                                                                                                                       /label= N-terminus
/note= "extracellular"
                                                                                                                                                                                                                                                                                                                                                                                                        'note= "transmembrane"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "transmembrane"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .97..222
|Tabel= E2
|note= "extracellular"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= 12
/note= "Cytoplasmic"
                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "cytoplasmic"
                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                    .T 2
W30297 standard; Protein; 380 AA.
                                                                                                                                                                                                                                                                                                                                                                                        59..85
/label= TMH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= TMH2
                                                    99.78;
                                                                                                                                                                                                                                                                                    W30297;
14-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label- E2
                                                                                                                                                                                                                                                                                                                                                                                                                         /label= 11
                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                            note=
                                                             Similarity
                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                      294;
                                                     Query Match
Best Local 3
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Per Selective activation of target cell expressing modified G protein per coupled receptor - allows control of cellular proliferation, per sepecially for amplification of transfected cells in gene therapy Example 1: Page 74-76: 117pp: English.

Comprises of protein comprises human kappa opioid receptor (KOR), a comprises: (1) introducing into the cell an neurotransmission. A novel method for selectively activating a target cell (TC) comprises: (1) introducing into the cell a nucleic acid sequence (CC (I) that expresses a G protein-coupled receptor (A) modified to be activated superiorly by a synthetic ligand (RASEL); and (ii) exposing the transfected cell to small synthetic modeleds (B) that corporase associated with receptor activation. (A) has: (a) tesponse associated with receptor activation. (A) has: (a) decreased binding affinity for a selected natural ligand of the native receptor: (b) binding affinity for (B); and (c) is activated by binding (B); sufficiently to produce the required cellular response. Also new are: (1) transgenic cells including the receptor of the genome; (2) cellular implants comprising a cellular product, particularly to response where (1); and (4) transfected with (1); (3) isolated (1); and (4) transfected with (1); (3) isolated (1); and (4) transfected with (1); (3) isolated (1); and contraction of a cellular product, particularly a heterologous therapeutic protein cellular product, particularly a heterologous therapeutic protein cellular product, particularly encoded by a second inserted nucleic acid sequence. Particularly con transfected during gene therapy procedures. Other responses that can be regulated are cell migration and contraction, or pigment contains a sequence animals, expression or stimulation of a second inserted contains a protein contains a production. In transgenic animals, expression or stimulation of a second inserted animals, expression or stimulation of a second inserted contains and contraction or pigment decaped to expend therapy procedures. Other responses 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 ytkmktatniyifnlaladalvtttmpfqstvylmnswpfgdvlckivisidyynmftsi 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YIKMKTAINIYIENLALADALVITIMPEQSIVYLMNSWPFGDVLCKIVISIDYYNMFTSI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "potential N-glycosylation"
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larity 97.6%; Pred. No. 2.86e-190;
Conservative 1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                /label= TMH7
/note= "transmembrane"
                                                                                                                     /label= TMH6
/note= "Transmembrane"
                                                                                                                                                                                                                                   /label= E3
/note= "Extracellular"
/label= I3
/note= "Cytoplasmic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= C-terminus
/note= "cytoplasmic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "palmitate"
                                                                              ..299
                                                                                                                                                                                               .311
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26-MAR-1996; US-622348.
(REGC ) UNIV CALIFORNIA.
CODALID BR;
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es 288; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 97-502739/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide_bond
Modified_site
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Matches
                                                                                          Domain
                                                                                                                                                                                                       Domain
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266
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ftltmmsvdryjavchpvkaldfrtplkakiiniciwllsssvgisaivlggtkvredvd 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                04-SEP-1996 (first entry)
Human kappa opioid receptor.
Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
neurology; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7: Page 13-15; 30pp; French.

The sequence coding for the human kappa opioid receptor was obtained from two overlapping CDNA fragments isolated from a human placental cDNA library. The fragments were amplified from the library using PCR primers based on the sequence of human genomic clones which hybridised with a murine delta receptor CDNA probe. Nucleotide probes derived from the kappa opioid receptor coding sequence are useful for diagnosis of neurological, cardiovascular and psychiatric disorders associated with opioid receptors. The receptor can be used for identifying e.g. agonists
                    181 XNLRRITRLVLVVVAVEVVCWTFIHIFILVEALGSTSHSTAALSSYYFCIALGYINSSLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XNLRRITRLVLVVVAVVAVFVVCWTPIHIFILVEALGSISHSTAALSSYYFCIALGXTNSSLN
                                                                         viecslqfpdddyswwdlfmkicvfifafvipvliiivcytlmilrlksvrllsgsrekd
                                                                                                                                                rnlrritrlvlvvvavfvvcwtpihifilvealgstshstaalssyyfcialgytnssln
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07-JUL-1995; FO0912.

11-JUL-1994; FR-008531.

(UYSI-) UNIV PASTEUR STRASBOURG LOUIS.

Kieffer B. Simonin F;

WPI: 96-097628/10.

N-PSDB: 712550.

New nucleic acid encoding the human Kappa opioid receptor - useful diagnosis and therapy, and for isolating receptor ligands and
                                                                                                                                                                                                                                     pilyafldenfkrcfrdfcfplkmrmergstsrvrntvqdpaylrdidgm-nkpv 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILYAPLDENEKRCFRDFCFPLKMXMERXSTSRVRNTVQDPAYLREIDGMMNKFV 295
                                                                                                                                                                                                                    pilyafldenfkrcfrdfcfplkmrmerqstsrvrntvqdpaylrdidgm-nkpv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 2192; DB 17; Length 380;
Pred. No. 2.86e-190;
1; Mismatches 5; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           its activity for potential use as analgesics usence 380 AA;
                                                                                                                                                                                                                                                                                                                                AA
                                                                                                                                                                                                                                                                                                                                R88722 standard; Protein; 380
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Best Local Similarity
Matches 288; Conser
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147
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Human kappa opioid receptor fusion polypeptide.
Selective target cell activation, G protein-coupled receptor;
RASSL, gene therapy, cell proliferation; Kappa opioid receptor;
human; transgenic animal; arrhythmia; bone disease; seizure;
vascular contraction; disease model.
Chimeric - Homo sapiens.
Chimeric - Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "human kappa opioid receptor"
                                                                                                                                                                                                                                                                                                              1..30
/label= Sig_peptide
/note= "prolactin signal sequence"
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382
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/note= "Extracellular"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= TMH1
/note= "transmembrane"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |70..191
|Tabel= TMH3
|note= "transmembrane"
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/label= E3
/note= "Extracellular"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= TMH4
/note= "transmembrane"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= TMH5
/note= "transmembrane"
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/note= "Transmembrane"
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/note= "transmembrane"
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/note= "extracellular"
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/note= "extracellular"
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|label= 12
|note= "Cytoplasmic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Il
/note= "cytoplasmic"
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/note= "cytoplasmic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Cytoplasmic"
RESULT

K W30208 standard; Protein; 427 AA. AC W30208;

DY W30208 tandard; Protein; 427 AA. AC W30208;

DY Human Kappa Opioid receptor fusion of Human Kappa Opioid receptor fusion of Human Kappa Opioid receptor fusion of Human Kappa Chimeric - Synthetic.

SC Chimeric - Synthetic.

FT Chimeric - Synthetic.

FT Rey Chimeric - Synthetic.

FT Peptide | 10.00 Sapiens.

FT Peptide | 10.00 Sapiens.

FT Peptide | 10.00 Sapiens.

FT Pomain | 10.00 | 10.00 | 10.00 |

FT Domain | 10.00 |

FT Do
                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Selective activation of target cell expressing modulined G protein coupled receptor - allows control of cellular proliferation, especially for amplification of transfected cells in gene therapy. Example 1: Page 77-79; IlTyp; English.

This polypeptide comprises the human G protein-coupled kappa opioid receptor (KOR) (see also W30297) flanked by N- and cellular sequences that facilitate the detection and purification of recombinant KOR, and especially KOR RASSIS (see W30299), i.e. a receptor activated superiorly by a synthetic ligand. A novel method for selectively activating a trayet cell (TC) comprises: (i) introducing into the cell a nucleic acid sequence (I) that expresses a RASSI (A) and (ii) exposing the transfected cell to small synthetic molecules (B) that bind to and activate (A), inducing the G protein coupled cellular response affinity for a selected natural ligand of the native receptor; (b) sociated with receptor activation. (A) has: (a) decreased binding affinity for a selected natural ligand of the native receptor; (b) binding affinity for (B); and (c) is activated by binding (B) sufficiently to produce the required cellular response. Also new are: transgenic cells including theterologous (I); in the genome; cellular implants comprising a TC transfected with (I); isolated (I); and transgenic cells including preceded with (I); isolated (I); and transgenic animals expressing (A). Activation of a cellular product, particularly a heterologous cells that are successfully transfected during gene therapy procedures. Other responses that can be regulated are cell contraction, or signment production. In transgenic animals, symptoms of bone disease, seizures, vascular contractions, dementia, neurodegeneration etc., for use as models contractions of improved food products (e.g. increased calcium ferrities of there inhure laborated active (E). In the second increased contraction of improved food products (e.g. increased column
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/note= "palmitate"
418..427
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97.6%;
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                                                /label= HA
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Conklin BR;
                                                                                                           25-MAR-1997; U05334.
26-MAR-1996; US-622348,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                            WPI; 97-502739/46.
N-PSDB; T90999.
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                              Peptide
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Transgenic animals defective in one type of opioid receptor - used to identify agents for treatment of pain, drug addiction and transplant rejection, lacking side effects of known opiate(s).

Disclosure; Fig 13, 58pp; French.

This sequence represents the mouse kappa opiate receptor. The gene sequence is used to generate a transgenic non-human mammal for identifying agents for treating disorders associated with opiate receptors. In the mammal, the expression of the gene encoding the opiate receptor is modified, particularly by the deletion of an exon and/or insertion of a marker gene, e.g. the neomycin resistance gene, into the sequence. Especially the expression of the gene is altered in nervous tissue. The agents are potentially useful for treating severe pain (chronic or acute), drug addiction and/or prevention or treatment of transplant rejection (as immunosuppressants). The method may isolate and identify powerful analgesics that lack morphine-like
                                                                                                    Mouse, kappa opiate receptor; transgenic animal; mammal; identification; exon; nervous tissue; pain; drug addiction; transplant rejection; immunosuppressant; analgesic; morphine; side effect.
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Mouse kappa optoid receptor mORK1.
Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify; transmembrane domain; somatostatin; receptor; human; expression vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 ytkmktatniyifnlaladalvtttmpfqsavylmnswpfgdvlckivisidyynmftsi 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 ftltmmsvdryiavchpvkaldfrtplkakiiniciwllassvgisaivlggtkvredvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 viecslqfpddeyswwdlfmkicvfvfafvipvliiivcytlmilr1ksvrllsgsrekd
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Pred. No. 5.22e-185;
13; Mismatches 7; Indels 1.
                                                                                                                                                                                                                    11-JUL-1997; F01282.
15-JUL-1996; FR-008810.
(CNRS) CENT NAT RECH SCI.
Dierich A, Kieffer BL, LeMeur M, Matthes HWD, Simonin FH;
WPI; 98-110582/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  truncate; chimaeric; assay; probe.
Mus musculus.
W09428132-A.
20-NAY-1994; U05747.
20-NAY-1993; US-066296.
T
W44939 standard; Protein; 380 AA.
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R67669 standard; Protein; 380 AA.
                                                              28-OCT-1998 (first entry)
Mouse kappa opiate receptor.
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                                                                                                polypeptides for useful drug substances.

For screening assays for useful drug substances.

Claim 8; Page 207-211; 300pp; English.

The amino acid sequence of the novel mouse kappa opioid receptor mork1.

The amino acid sequence of the novel mouse kappa opioid receptor mork1.

The amino acid sequence of the novel mouse brain copy library using a fragment (amplified from the conserved sequences present in the copies. The primers are based on the conserved sequences present in the comber. The primers are based on the conserved sequences present in the comber. The primers are based on the conserved sequences present in the couptor subtypes SSTR1, SSTR2 and SSTR3. The 1.2 kb Pst1 fragment from the mouse kappa opioid receptor clone, lambda msl-1, was subcloned into the CMV copy promoter-based expression vector pcWV-6b. The resultant construct pcWV-msl-1 was transfected into COS-1 cells for protein production. The gene encoding the opioid receptor can be used to produce complete.

Crumcated or chimacric opioid receptor proteins. The opioid receptors thus produced are useful for the development of novel assays designed to select or improve substances, capable of interacting with the opioid receptor protein says designed to receptor proteins, for use in diagnosis, drug design and therapeutic
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mammalian kappa opioid receptor protein.
Mammalian kappa opioid receptor: mouse delta opioid receptor; analgesic; amplification; primer; rat; probe; E.coli; RT-PCR; hypnotic compound; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kappa opioid receptor protein and cells expressing it - useful for the screening of compounds for analgesic and hypnotic
                                                                                                                                                                                                                                                                                                                                                                                                      Score 2136; DB 13; Length 380;
Pred. No. 5.22e-185;
13; Mismatches 7; Indels 1
30-JUL-1993; US-100694.
(NS-NOV-1993; US-17592.
(ARCH-) ARCH DEV CORP.
Bell GI, Reisine I, Yasuda K;
WHI, 95-02804/03.
N-PSDB: Q75926.
Polynucleotides and peptides derived from opioid receptor
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111..1253
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92.9%;
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WPI; 95-144857/19.
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30-JUL-1993; 190261.
09-JUL-1993; JP-170591.
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274; Conser
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N-PSDB; Q86725
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Claim 2; Page 9-10; 15pp; Japanese.

The amino acid sequence of the novel mammalian kappa opioid receptor. The amino acid sequence of the novel mammalian kappa opioid receptor. The gene was isolated by amplifying a fragment from rat brain mRnA by reverse transcriptase-PCR (RT-PCR) using primers Q86726-7 derived from the mouse delta-opioid receptor gene. This fragment was aloned into the plasmid pRII to produce pRII. The plasmid pRII was used to probe a rat brain DNA library in lambda ZAPII to obtain a clone of the rat kappa opioid receptor gene, designated pKOPR2. This clone was introduced into E.coli JM109 for production of the receptor protein. The receptor protein peptides and proteins.
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Pred. No. 1.24e-184;
13; Mismatches 8; Indels 1.
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Pred. No. 1.24e-184;
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WPI; 95-275452/36.
New DNA encoding human mu opiate receptor
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
(USSH ) US SEC DEPT HEALTH.
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92.5%;
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Kappa opiate receptor; mu
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30-JAN-1995; U01144.
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FILTMMSVDRYIAVCHPVKALDFRTPLKAKIINICIWLLSSSVGISAIVLGGTKVREDVD 120
                                                                    181 XNLRRITRLVLVVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLN
                                                  viecslgfpddeyswwdlfmkicvfvfafvipvliiivcytlmilrlksvrllsgsrekd
rnlrritklvlvvvavfiicwtpihifilvealgstshstavlssyyfcialgytnssln
                                                                                                                                                                                         pvlyafldenfkrcfrdfcfpikmrmergstnrvrntvqdpasmrdvggm-nkpv 380
                                                                                                                                                                                                             14-APR-1998 (first entry)

Human Kappa opioid receptor RASSL ORL.

Selective target cell activation; G protein-coupled receptor;

RASSL; gene therapy; cell proliferation; kappa opioid receptor;

human; transgenic animal; arrhythmia; bone disease; seizure;

vascular contraction; disease model.

Chimeric - Homo saplens.

Chimeric - Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "extracellular, contains 17 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             residues from delta opiod receptor (Val.235, Gln-237, Pro-238, Asp-240, Gly-241, Ala-242, Val-243, Val-244, Thr-246, Ser-251, Pro-252, Ser-253, Thr-224, Tyr-255, Thr-259, Thr-260)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "human kappa opioid receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Sig_peptide
/note= "prolactin signal seguence"
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/label= TMH4
/note= "transmembrane"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39..95
/label= N-terminus
/note= "extracellular"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "transmembrane"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "transmembrane"
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/note= "transmembrane"
282..309
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/note= "cytoplasmic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Cytoplasmic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                              n 9
W30299 standard; Protein; 424 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label= FLAG
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/label= TMH1
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/label= KOR
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/label= E
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NPSDB 79-502739/46.

BR NPSDB 79-502739/46.

RNP: 97-502739/46.

PR Selective activation of target cell expressing modified G protein coupled receptor - allows control of cellular proliferation.

PR Selective activation of transfected cells in gene therapy shample 1: Page 80-82. 117pp. Bnglish.

PR SEAMPLE 1: Page 80-82. 117pp. Bnglish.

CC This protein coupled kappa opioid receptor (KCR) (see also W30297)

CC modified at 17 amino acid positions to contain the corresponding amino acid of the delta opioid receptor (KCR) (see also W30297)

CC Terminal flanking sequences that facilitate the detection and purification of recombinant protein. A movel method for selectively activating a target cell (TC) comprises: (1) introducing into the cull and (ii) exposing the transfered cell to small synthetic molecules (B) that bind to and activate (A), inducing the G protein coupled cellular response associated with receptor activation. (A) has: (a) decreased binding affinity for (B); and (C) is activated cellular implants comprising a TC transfected with (I); collular response.

Also new are: transgenic cells including heterologous (I) in the compressing (A) results, in vitro or in vivo, in cellular product, particularly a heterologous (I) in the response. Collular product he relatively few collular and that are successfully transfected duting few cells that are successfully transfected duting few cells cells and cellular product, particularly and cell cellular product. Particularly and cellular product. Particularly and cellular product. Particularly few cells cellular product and cellular product particularly decreased cellular product. Particularly decreased cellular product cellular product particularly decreased cellular product particularly decreased cellular product. Particularly decreased cellular product particularly decreased cellular product particularly decreased cellular product partic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       procedures. Other responses that can be regulated are cell migration and contraction, or pigment production. In transgenic animals, expression or stimulation of (A) is designed to develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
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Pred. No. 5.44e-173;
4; Mismatches 18; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "potential N-glycosylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "potential N-glycosylation"
                                                                                                      /label= TMH6
/note= "Transmembrane"
                                                                                                                                                                                                                /label= E3
/note= "Extracellular"
                                                                                                                                                                                                                                                                                                                          /label= TMH7
/note= "transmembrane"
                                                                                                                                                                                                                                                                                                                                                                                                                         /label= C-terminus
/note= "cytoplasmic"
168..245
                              "Cytoplasmic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "palmitate"
415..424
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Best Local Similarity 91.2%;
Matches 269; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415..424
/label= HA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             content in eggshells or alfertility or induce labour
/label= I3
                                                                .333
                                                                                                                                                                                                                                                                                ..367
                                                                                                                                                                                                                                                                                                                                                                                              368..414
                                                                                                                                                                              334..345
                                  'note=
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181 XNLRRITRLVLVVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFCIALGYINSSLN 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transgenic animals defective in one type of opioid receptor - used transgenic animals defective in one type of opioid receptor - used transgenic for treatment of pain, drug addiction and transplant rejection, lacking side effects of known opiate(s) bisclosure; Fig 11; 58pp; French.

This sequence represents the mouse mu opiate receptor. The gene sequence is used to generate a transgenic non-human mammal for identifying agents for treating disorders associated with opiate receptors. In the mammal, the expression of the gene encoding the opiate receptor is modified, the expression of the gene encoding the opiate receptor is modified, gene, e.g. the neonycin resistance gene, into the sequence. Especially the expression of the gene is altered in nervous tissue. The agents are potentially useful for treating severe pain (chronic or acute), drug addiction and/or prevention or treatment of transplant rejection (as immunosuppressants). The method may isolate and identify powerful
                                                                                                                                                                                                   300
                                                                                                                                                                                                                                                                                                    360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse, mu opiate receptor; transgenic animal; mammal; identification; exon; nervous tissue; pain; drug addiction; transplant rejection; immunosuppressant; analgesic; morphine; side effect.
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                                               YIKMKTATNIYIFNLALADALVITTMPFQSTVYLMNSWPFGDVLCKIVISIDYYNMFTSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUL-1997; F01282.
15-JUL-1996; FR-008810.
CURS) CENT NAT RECH SCI.
Dierich A, Kieffer BL, LeMeur M, Matthes HWD, Simonin FH;
WPI; 98-110582/10.
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W44937 standard; Protein; 398
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hes 190; Conser
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28-OCT-1998
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Claim 2: Fig 9; 39pp; English.

Claim 2: Fig 9; 39pp; English.

R65188 is the rat mu-subtype opioid receptor protein purified from rat brain membranes, with biotinyl-b-endorphin (R6666) as its ligand. It is encoded by the nucleotide sequence 079199 which was synthesised using 071022 and 071023 as PCR primers.

R65188 is useful for identifying othe receptor subtypes, for screening new opioid ligands, and for studying mechanisms of
                                                                                                                                                                                                                                                                                                                    'note≈ "Threonine residue especially favourable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pure mu-type opioid receptor protein - and nucleic acid coding
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/note= "hydrophobic membrane spanning
139.166
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                                                                                                                                                                                                                                                                                                                                      for protein kinase A phosphorylation"
                                                                                                                                                                           Murine mu-subtype opioid receptor.
Mu-subtype opioid receptor; MSOR; drug addiction.
Rattus rattus.
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Pred. No. 1.78e-127;
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                                                                                                                   R65188 standard; Protein; 356 AA.
R65188;
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Corbett MJ, Eppler CM, Shie
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larity 66.1%;
Conservative
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187..212
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274..294
/note= "h;
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/note= '
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26-FEB-1993; US-026140.
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Best Local Similarity
Matches 191; Conser
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N-PSDB; Q79199.
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Rattus sp.
WO9507983-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                      156 ftlctmsvdryiavchpvkaldfrtprnakivnvcnwilssaiglpvmfmattkyrgg-s 214
                                                                                                                                                                                                                                                                                                                                                                                                 1 YIKMKTATNIYIFNLALADALVTTTMPFQSTVYLMNSWPFGDVLCKIVISIDYYNMFTSI 60
                                                                                                                                                                                                                                 New DNA encoding human mu opiate receptor - used esp. for screening cpds. for activity as opiate agonists or antagonists Disclosure; Page 26-28; 49pp; English.

HWOR CDNA was obtd. from a human cerebral cortical cDNA library screened with fragments of a rat mu opiate receptor. The encoded protein showed homology to rat mu, delta and kappa opiate receptors (R76781-83).
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -idctltfshptw-ywenllkicvfifafimpvliitvcyglmilrlksvrmlsgskekd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding new human mu opioid receptor - and related vectors, transformed cells, antibodies etc., useful in
                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                       Rat mu opiate receptor. Mu opiate agonist; opiate antagonist; drug abuse; analgesic.
                                                                                                                                                                                                                                                                                                                                 Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pvlyafldenfkrcfrefciptsstieggnstrvrgntrehpstantvd 339
                     pvlyafldenfkrofrefciptsstieggnstrvrgntrehpstantvd 381
                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                      45; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                  Score 1522; DB 14;
Pred. No. 1.78e-127;
                                                                                                                                                                                                                 Wang J;
                                                                                                                                                         03-AUG-1995.
28-JAN-1995; U01144.
28-JAN-1994; US-188275.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
(USSH) US SEC DEPT HEALTH.
Johnson PS. Persico AM, Uhl G, Wang J
                                                                          AA.
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R71966;
                                                                T 12
R76781 standard; Protein; 398
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Best Local Similarity 66.1%;
Matches 191; Conservative
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13-SEP-1994; U10358.
13-SEP-1993; US-1206
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WPI; 95-131351/17.
                                                                                                                                                                                                                                                                                                               398 AA;
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                                                                                                                                                  W09520667-A1.
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W09507983-A
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                                                                                                                                         Rattus sp.
                                                                                                                                                                                                                                                                                                               Sequence
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Disclosure; Page 190-194; 266pp; English.
A 365 bp fragment of the mouse delta opioid receptor was used to screen a rat brain cDNA library under low stringency conditions. One positive clone included the sequence given in Q89222, encoding mu opioid receptor, MOR-1 (R71964). MOR-1 was stably expressed in Sequence 398 AA;
                                                                                                                                ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 ftlctmsvdryiavchpvkaldfrtprnakivnvcnwilssaiglpvmfmattkyrgg-s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 ftlctmsvdryiavchpvkaldfrtprnakiinvcnwilssaiglpvmfmattkyrgg-s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 -idctltfshptw-ywenllkicvfifafimpvliitvcyglmilrlksvrmlsgskekd
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YTKMKTATNIYIFNLALADALVTTTMPFQSTVYLMNSWPFGDVLCKIVISIDYYNMFTSI
diagnosis, treatment and drug screening.

Claim 4; Page 211-214; 266pp; English.
A cDNA library constructed from human caudate nucleus mRNA was screened with rat mu opioid receptor cDNA under conditions of low stringency. One positive clone included the sequence given Q89226, encoding a mu opioid receptor MOR (R71964). The cDNA is used for prodn. of recombinant MOR, in gene therapy, etc. Sequence 400 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding new human mu opioid receptor - and related vectors, transformed cells, antibodies etc., useful in
                                                                                                                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                                                                   Length 400;
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Rat mu opioid receptor.
Mu opioid receptor; MOR-1; gene therapy; diagnostic.
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Pred. No. 2.73e-127;
46; Mismatches 49;
                                                                                                                                                                                                                                                                      Score 1522; DB 13;
Pred. No. 1.78e-127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
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65.7%;
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(INDV ) UNIV INDIANA FOUND.
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Local Similarity 67.1%;
es 188; Conservative
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N-PSDB; Q89222.
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PARA-1994; US-188275.

A (USSH) 10 S DEPT HEALTH.

A (USSH) 10 S DEPT HEALTH.

Johnson PS. Persico AM, Uhl G, Wang J;

NR WPI; 95-275452/36.

N-PSDB; 093102.

New DNA encoding human mu opiate receptor - used esp. for screening cpds. for activity as opiate agonists or antagonists of claim 1; Page 25-26; 49pp; English.

HORS DNA WAS obtd. from a human cerebral cortical cDNA library creened with fragments of a rat mu opiate receptor. Expression of hMORI in COS cells revealed high affinity recohnition of the mu opiate specific ligand. Recombinant hMORI can be used to screen
                                                                                                                    240
                        180
                                                                     332
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                                                                   273 rnlrritrmvlvvvavfivcwtpihiyviikalitipettfqtvswhfcialgytnscln
                                                                                              Score 1520; DB 14; Length 400;
Pred. No. 2.73e-127;
43; Mismatches 46; Indels 3;
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Human mu opiate receptor.
Mu opiate receptor; hMOR; opiate agonist; opiate antagonist;
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		1 3-08-149 xxxxx	ednence 7	Sequence 7, Application US/081 Patent No. 5658783 GENERAL INFORMATION: APPLICANT: Bunzow, James R APPLICANT: Grandy, David K TITLE OF INVENTION: Opioid NUMBER OF SEQUENCES: 7 CORRESPONDENCES: 7 ADDRESSE: ADDRESSE: ADDRESSE: ADDRESS: ADDRESSE: ADDRESS: ADDRESSE: ADDRESS: ADDRESSE: ADDRESS: ADDRESSE: Banner & Alle STREET: 111nnois . COMPUTER: USA ZIP: 6066 COMPUTER READABLE FORM: APPLICATION SYSTEM: PC-DOS SOFTWARE: PATENTIN RE-DOS CORPUTER: PALCATION DATA: APPLICATION NUMBER: US/0 FILING DATE: 06-NOV-1993 CLASSIFICATION: 45-1000 TELESY 100-5658783nan, KE RESIERRALION NUMBER: 35- ATTORNEY/AGENT INFORMATION: MAME: NO. 5658783nan, KE RESIERRALION FOR STELLONO TELESAX: 312-715-1000 TELEFAX: 312-715-1234 INFORMATION FOR SEQ ID NO: 7 SEQUENCE CHARACTERISTICS: LENGTH: 380 amino acids TYPE: amino acid
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FEATURE:
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APPLICANT: Bunzow, James R
APPLICANT: Bunzow, Javid K
APPLICANT: Grandy, David K
TITLE OF INVENTION: A No. 5821067el Mammalian Methadone-Specific
TITLE OF INVENTION: Opioid Receptor Gene and Uses
                                                                                                                   87 YTKMKTAINIYIFNLALADALVTITMPFQSAVYLMNSWPFGDVLCKIVISIDXYNMFTSI 146
                                                                                                                                                                                                                                                           181 XNLRRITRLVLVVVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLN 240
                                                                                                                                                             147 FILTMMSVDRYIAVCHPVKALDFRTPLKAKIINICIWLLASSVGISAIVLGGTKVREDVD 206
                                                                                                                                                                          61 FILTHMSVDRYIAVCHPVKALDFRTPLKAKIINICIWILSSSVGISAIVLGGTKVREDVD 120
                                                                                                                                                                                                      207 VIECSLQFPDDEYSWWDLFWKICVFVFAFVIPVLIIIVCYTLMILRLKSVRLLSGSREKD 266
                                                                                                                                                                                                                   267 RNLRRITKLVLVVVAVFIICWTPIHIFILVEALGSTSHSTAALSSYYFCAILGYTNSSLN 326
                                                                                                                                  1 YTKWKTAINIYIENLALADALVITIMPFQSTVYLMNSWPFGDVLCKIVISIDIYNMFISI 60
                                                                                                1; Gaps
                                                                                                                                                                                                                                                                                                      327 PVLYAFLDENFKRCFRDFCFPIKMRMERQSINRVRNTVQDPASMRDVGGM-NKPV 380
                    LOCATION: 1..380
OTHER INFORMATION: /label- Identifier
OTHER INFORMATION: /note= "Mouse Kappa-Opioid Receptor"
NCE 380 Ab, 42652 MW; 802929 CN;
                                                                          Score 2123; DB 1; Length 380; Pred. No. 1.68e-175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TRYPE: RIOPPY disk
COMPUTER: IRM PC compatible
COMPUTER: IRM PC compatible
CORPUTARE: Patentin Release #1.0, Version #1.25
SUFRARE: Patentin Release #1.0, Version #1.25
RURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,245
FILING DATE: 15-AUG-1997
                                                                                                9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
CITY: Lillinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                          380 AA
                                                                                               13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149093
FILING DATE: 06-NOV-1993
ATTORNEY/AGRWT INFORMATION:
NAME: No. 5821067nan, Kevin E
REGISTRALTON NUMBER: 35.33
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08911245
Patent No. 5821067
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08911245
                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                          Query Match
Best Local Similarity 92.2%;
Matches 272; Conservative
          NAME/KEY: Protein
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US-08-911-245-7
                                                    SEQUENCE
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Gaps 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 RNLRRITKLVLVVVAVFIICWTPIHIFILVEALGSTSHSTAALSSYYFCAILGYTNSSLN 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 FILTMMSVDRYIAVCHPVKALDFRTPLKAKIINICIWLLASSVGISAIVLGGTKVREDVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 VIECSLQFPDDEYSWWDLFMKICVFVFAFVIPVLIIIVCYTLMILRLKSVRLLSGSREKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        327 PVLYAFLDENFKRCFRDFCFPIKMRMERQSTNRVRNTVQDPASMRDVGGM-NKPV 380
                                                                                                                                                                                                                                                                                                                                                                                               Score 2123; DB 2; Length 380;
Pred. No. 1.68e-175;
13; Mismatches 9; Indels 1;
                                                                                                                                                                                                                                                                                                   RINFORMATION: /label= Identifier
SINFORMATION: /note= "Mouse Kappa-Opioid Receptor"
380 AA, 42552 MM; 802929 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/08514451A
Patent No. 5837809
GENERAL INFORMATION:
APPLICANT: Bursow, James R.
APPLICANT: Grandy, David K.
APPLICANT: Civelli, Olivier
APPLICANT: Relines Monsma, Referr, Hans-Peter
APPLICANT: Monsma, Frederick J.
APPLICANT: Monsma, Frederick J.
TILLE OF INVENTION: A NOVEL MAMMALIAN OPIOID
TITLE OF INVENTION: RECEPTOR LIGAND AND USES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELES: 910-221-5317
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                              380 amino acids
                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acid
TYPE: amino acid
                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 92.2%;
Matches 272; Conservative
                                                                                                                                                                                                                                               NAME/KEY: Protein LOCATION: 1.380 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                               linear
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ORIGINAL SOURCE:
      COUNTRY: USA
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PCT-US94-10358-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 FTLINMSVDRYIAVCHPVKALDFRTPLKAKIIWICIWLLASSVGISALVLGGTKVREDVD 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206 VIECSL-FPDDEYSWWDLFMKICVFVFAFVIPVLIIIVCYTLMILRLKSVRLLSGSRKKD 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               265 RNLRRITKLVLVVVVAVFIICNTPIHIFILVEALGSTSHSTAALSSYYFCIALGYTMSSLM 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YTKMKTATNIYIFNLALADALVTTTMPFQSTVYLMNSWPFGDVLCKIVISIDYYNMFTSI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: EPPLER, C. Mark
APPLICANT: OZENBERGER, Bradley A.
APPLICANT: OLIMBS, Jeffrey D.
TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325 PVLYAFLDKNFKRCIRDFCFPIKMRMERQSINRVRNIVQDPASMRDVGGM-NKPV 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1990; DB 2; Length 378;
Pred. No. 1.25e-163;
15; Mismatches 15; Indels
                                                                    FILING DATE: 08/11/95
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/553,058
FILING DATE: 11/13/95
ATORNEY/AGENT INPORMATION:
NAME: William D. No. 5837809nan, M.D.
REGISTRATION NUMBER: 30,878
REPRENCE/POCKET NUMBER: 899-45995/WDN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391 AA
                                                           APPLICATION NUMBER: US/08/514,451A
FILING DATE: 08/11/95
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DESCRIPTION: peptide
ICE 378 AA; 42392 MW; 806199 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, P.C. STREET: 805 Third Avenue
CIIY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08454549
Patent No. 5866324
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08454549
                   SOFTWARE: WP5.1 ASCII text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 378 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 88.8%;
Matches 262; Conservative
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE IYPE:
                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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Sequence 8, Application PC/TUS9410358
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MU OPICID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 YTKMKTATNIYIFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSI 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILCIMSVDRYIAVCHPVKALDFRIPRNAKIVNVCNWILSSAIGLPVMFMATTKYRQG-S 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 -IDCTLIFSHPTW-YWENLLKICVFIFAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YTKMKTATNIYIFNLALADALVITTMPFQSTVYLMNSWPFGDVLCKIVISIDYYNMFTSI
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                                       MEDIDW TYPE: FILPSPY disk
COMPUTER: IBM PC COMPatible
COMPUTER: IBM PC COMPatible
COMPUTER: IBM PC COMPatible
COMPUTER: IBM PC COMPatible
CORRENT SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,549
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RODINSON, USSEPH R.
REGISTRALION NUMBER: 33,448
RESISTRALION NUMBER: 33,448
RESISTRALION NUMBER: 33,448
RESISTRANCATION NUMBER: 33,448
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LEMOTH: 391 anhino acids
STRANDEDNESS: not relevant
TYPE: annino acids
STRANDEDNESS: not relevant
MOTEGATIF MOTIFICATION
TO TELEVANTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1522; DB 2; L. Pred. No. 6.69e-122; 45; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NISM: Rat
391 AA; 43814 MW; 846718 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application PC/TUS9410358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.1%;
Matches 191; Conservative
ZIP: 10022
COMPUTER READABLE FORM:
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273 RNLRRITRWYLVVVAVFIVCWTPIHIYVIIKALITIPETTFQTVSWHFCIALGYTNSCLN 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 FILCTMSVDRYIAVCHPVKALDFRIPRNAKIVNVCNWILSSAIGLPVMFMAITKYRQG-S 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 YIKMKTAINIYIFNLALADALAISTLPFQSVNYLMGTWPFGTILCKIVISIDYXNMFTSI 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 -IDCTLIFSHPTW-YWENLLKICVFIFAFIMPILITTVCYGLMILRLKSVRMLSGSKEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 68.2%; Score 1520; DB 1; Length 398; Best Local Similarity 65.7%; Pred. No. 1.01e-121; Matches 190; Conservative 46; Mismatches 49; Indels
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OTHER INFORMATION: /label= Identifier
OTHER INFORMATION: /note= "Rat Mu-Opioid Receptor"
NCE 398 AA; 44508 MW; 870781 CN;
                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT MANUMERR: US/08/149,093A
FILING DATE: 06-NOV-1993
                            ADDRESSER Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
CITY: Lilinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              398
                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Patent No. 5821067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08911245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein FEATURE:
                                                                                                                                                     COMPUTER READABLE FORM:
              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: ] ; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Protein
                                                                                                                                   90909
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Patent No. 5558783
GENERAL INFORMATION:
APPLICANT: Bunzow, James R
APPLICANT: Grandy, David K
TITLE OF INVENTION: A No. 5558783el Mammalian Methadone-Specific
TITLE OF INVENTION: Opioid Receptor Gene and Uses
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -IDCTLTFSHPTW-YWENLLKICVFIFAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKD: 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 YTKMKTATULYIFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             275 RNLRRITRAVLVVVAVEIVCWTPIHIYVIIKALVTIPETTFQTVSWHFCIALGYINSCLN 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 68.3%; Score 1522; DB 3; Length 400; Local Similarity 67.1%; Pred. No. 6.69e-122; les 188; Conservative 43; Mismatches 46; Indels
                                                               COMPUTER FRANCHE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: FLOP disk
COMPUTER: FLOP MISK
COMPUTER: FLOP MISK
COMPUTER: FLOP MISK
COMPUTER: PATENTIN FELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: COLUTION HERWITH HERWITH PERSISTICATION:
PRIOR APPLICATION:
PRIOR DATE: 13 SEPTEMBER 1993
ATTORNEY/ACENT INDORMATION:
PRILING DATE: 13 SEPTEMBER 1993
ATTORNEY/ACENT INDORMATION:
REGISTRATION NUMBER: 37,259
REFERENCE/POCKET NUMBER: INDA005P--
TELEPHONE: 512 ATR 9-2679
TELEPHONE: 612 ATR 9-2679
TELEFX: 79-0924
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CARRACTERISTICS:
LENGTH: 400 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           335 PVLYAFLDENFKRCFREFCIPTSSNIEQQNSTRIRQNTRD 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
JENCE 400 AA; 44779 MW; 873826 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08149093A
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STATE: 16. COUNTRY: USA 77210
                  Texas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Gaps

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Sequence 2, Application PC/TUS9410358
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STRIE: Texas
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YTKMKTATNIY1FNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSI 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILCIMSVDRYIAVCHPVKALDFRIPRNAKIVNVCNWILSSAIGLPVMFMATIKYRQG-S 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273 RNLRRITRMVLVVVAVFIVCWTPIHIYVIIKALITIPETTFQTVSWHFCIALGYTNSCLN 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 -IDCTLTFSHPTW-YWENLLKICVFIFAFIMPILLITVCYGLMILRLKSVRMLSGSKEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 398;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 68.2%; Score 1520; DB 3; L
Best Local Similarity 65.7%; Pred. No. 1.01e-121;
Matches 190; Conservative 46; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: CONCURRENTLY herewith CLASSIFICATION:
PRIOR APPLICATION DATE: APPLICATION DATE: APPLICATION NUMBER: 08/120.601
FILING DAIE: 13 SEPIEMBER 1993
ATTORNEY, PAGENT INFORMATION:
NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REGISTRATION NUMBER: 37,259
REFERENCE/POCKET NUMBER: INDA005P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 418-3000
TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
SEQUENCE 398 AA; 44508 MW; 870781 CN;
                                                                                Sequence 2, Application PC/TUS9410358
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TELEX: 79-0924
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 FILCIMSVDRYIAVCHPVKALDFRIPRNAKIVNVCNWILSSAIGLPVWFMATIKYRQG-S 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273 RNLRRITRMVLVVVVAVFIVCWIPIHIYVIIKALITIPETTFQTVSWHFCIALGYTNSCLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215 -IDCTLTFSHPTW-YWENLLKICVFIFAFIMPILIITVCYGLMILRLKSVRMLSGSKEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
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Pred. No. 1.01e-121;
46; Mismatches 49; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Protein
LOCATION: 1.398
OIDER INFORMATION: /label= Identifier
OIHER INFORMATION: /note= "Rat Mu-Opioid Receptor"
NCE 398 AA: 44508 MW; 870781 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 PILYAFLDENFKRCFRDFCFPLKMXMERXSTSRVR-NTVQDPAYLREID
                                              A No. 5821067el Mammalian Met.
Opioid Receptor Gene and Uses
                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                         ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: 1111nois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              398
                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: Journal PRIOR APPLICATION NUMBER: US 08/149093
FILING DATE: 06-NOV-1993
ATORNEY/AGENT INFORMATION:
NAME: No. 5821067nan, Kevin E REGISTRATION NUMBER: 35,303
REPRENCE/DOCKET NUMBER: 93,311
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEPHONE: 312-715-1000
TELEPRAS: 312-715-1000
TELEPRAS: 910-211-5317
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                  FILING DATE: 15-AUG-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                 James R
David K
                                                                                                                                                                                        ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 398 amino acids amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                              NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 68.2%;
Local Similarity 65.7%;
les 190; Conservative
                                              TITLE OF INVENTION:
               APPLICANT: Bunzow, APPLICANT: Grandv,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
GENERAL INFORMATION:
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ID PCT-US94-10358-2
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Q_{\overline{A}}
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'Atent No. Johnson
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brandy, David K
APPLICANT: Grandy, David K
TITLE OF INVENTION: A No. 5821067el Mammalian Methadone-Specific
TITLE OF INVENTION: Opioid Receptor Gene and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 FILTMMSVDRYIAVCHPVKALDFRTPAKAKLINICIWVLASGVGVPIMVMAVTQPR-DFA 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YIKMKIAINIYIENLALADALVITIMPEQSIVYLMNSWPFGBVLCKIVISIDYXNMFISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1..372
OTHER INFORMATION: /label= Identifier
OTHER INFORMATION: /note= "Mouse Delta-Opioid Receptor"
NCE 372 AA: 40617 MW; 728086 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1451; DB 2; Length 372
Pred. No. 1.37e-115;
42; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,245
FILING DATE: 15-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B: Banner & Allegretti, Ltd.
10 South Wacker Drive, Suite 3000
                                                                                                                         372 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: C.C. CLASSIFICATION: CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/149093
FILING DATE: 06-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5821067nan, Kevin E
NAME: No. 5821067nan, Kevin E
NAME: No. 5821067nan, Revin E
NAME: 
                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08911245 Patent No. 5821067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 93,3
TELECOMMUNICATION INFORMATION:
TELEFAX: 312-715-1034
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 372 anino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                       Sequence 6, Application US/08911245
240 NPILYAFLDENFKRCFRDFC 259
                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 69.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 10 South
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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                                                                                                                      US-08-911-245-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VV-CILQFPSPSW-YWDIVIKICVFLFAFVVPILIIITVCYGLMLLRLRSVRLLSGSKEKD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 RSLRRITRMVLVVVGAFVVCWAPIHIFVIVWTLVDINRRDPLVVAALHLCIALGYANSSL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 FILTMMSVDRYIAVCHPVKALDFRTPAKAKLINICIWVLASGVGVPIMVMAVTQPRDGA- 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YTKMKTAINIYIFNLALADALVITTMPFQSIVYLMNSWPFGDVLCKIVISIDXYNMFTSI 60
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                                                                                                                                                                                                                                                                    APPLICANT: EPPLER, C. Mark
APPLICANT: OZENBERGER, Bradley A.
APPLICANT: OZENBERGER, Bradley A.
APPLICANT: HUMBS, Jeffrey D.
TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
TITLE OF INVENTION: TO OPICID RECEPTORS
CORRESPONDENCE: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,549
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURREAL APPLICATION APPLICATION 435
FILING DATE: 30-12.
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RODINGON, USED, S3,448
REGISTRATION NUMBER: 0646/1A818-US5
TELEPHONE: (212) 527-7700
TELEPHONE: (212) 527-7700
TELEPHONE: (212) 53-6237
TO A COMMUNICATION INFORMATION:
TELEPHONE: (212) 53-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1452; DB 2; I
Pred. No. 1.12e-115;
44; Mismatches 33;
367 AA.
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ICE 367 AA; 40122 MW; 712609 CN;
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Darby & Darby, P.C. STREET: 805 Third Avenue CITY: New York STATE: New York
                                                                                                                                                                                            Sequence 4, Application US/08454549 Patent No. 5866324 GENERAL INFORMATION:
                                                                                                                                              Sequence 4, Application US/08454549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SS: not relevant not relevant
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LENGIH: 367 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                314 NPVLYAFLDENFKRCFRQLC 333
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MOLECULE TYPE: protein
ORIGINAL SOURCE:
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Best Local Similarity 68.8%;
Matches 179; Conservative
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US-08-454-549-4
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Patent No. 5558783
GENERAL INFORMATION:
APPLICANT: Bunzow, James R
APPLICANT: Bunzow, David R
APPLICANT: GINZETION:
TITLE OF INVENTION:
TITLE OF INVENTION: Opioid Receptor Gene and Uses
             196 VV-CMLQFPSPSW-YWDTVTKICVFIFAFVVPILIITVCYGLMLLRLRSVRLLSGSKEKD 253
                                             254 RSLRRITRMVLVVVGAFVVCWAPIHIFVIVWTLVDINRRDPLVVAALHLCIALGYANSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Identifier
/note= "Mouse Delta-Opioid Receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1451, DB 1; Length 372,
Pred. No. 1.37e-115,
42; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Banner & Allegretti, itd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STAIE: Illinois
COUNTRY: USA
                                                                                                                                                                    372 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/149,093A FILING DATE: 06-NOV-1993 CLASSIFICATION: 435
                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: No. 568783tan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,311
                                                                                                                                                                                                                                          Sequence 6, Application US/08149093A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 312-715-1000
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TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 372 amino acids amino acids
                                                                                                                                                                    STANDARD;
                                                                                                           240 NPILYAFLDENFKRCFRDFC 259
                                                                                             314 NPVLYAFLDENFKRCFRQLC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE IYPE: protein
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Best Local Similarity 69.6%;
Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1..372 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Protein
LOCATION: 1..372
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                                                                                                                                                                   US-08-149-093A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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Gaps

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77 YTKLKTATNIYIFNLALADALATSTLPFQSAKYLMETWPFGELLCKAVLSIDYXNMFTSI 136

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: EVANS, CHRISTOPHER J.

APPLICANT: EDARROS, ROBERT H.

TITLE OF INVENTION: EXPRESSION CLONING OF A DELTA OPICID

TITLE OF INVENTION: EXCEPTOR, RELAIED EXPRESSION SYSIEMS, AND RELAIED

TITLE OF INVENTION: PHARMACEUTICALS

NUMBER OF SEQUENCES: 15

CORRESSONERICE ADDRESS:
                                                            FILTMMSVDRYIAVCHPVKALDFRTPAKAKLINICIWVLASGVGVPIMVMAVTQPR-DFA 195
                                                                                                                  FTLTMMSVDRYIAVCHPVKALDFRTPLKAKIINICIWLLSSSVGISAIVLGGTKVREDVD 120
                                                                                                                                                                                                                  254 RSLRRITRMVLVVVGAFVVCWAPIHIFVIVWTLVDINRRDPLVVAALHLCIALGYANSSL 313
                                                                                                                                                                                                                                                                                                                                       1 YTKMKTAINIYIFNLALADALVITTMPFQSIVYLMNSWPFGDVLCKIVISIDYYNMFTSI 60
                                                                                                                                                                               VV-CMLQFPSPSW-YWDIVIKICVFIFAFVVPILIITVCYGLMLLRLRSVRLLSGSKEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATIVE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372 AA.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/929,200
FILING DATE: 13.AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/411,859
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FENCE 372 AA; 40565 MW; 726402 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08411859 Patent No. 5985600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08411859
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-613-5600
TELEFAX: 415-494-0792
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: LITHGOW, TIMOTHY REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                             314 NPVLYAFLDENFKRCFRQLC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 NPILYAFLDENFKRCFRDFC 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
STATE: California
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Sequence 2, Appli
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C Sequence 2, Appli
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C Sequence 2, Appli
XX
C GENERAL INFORMA
CC GENERAL INVE
CC GENERAL INVE
CC TITLE OF INVE
CC ADDRESPONDEN
CC CONDUTER: Qa
CC CONDUTER: Qa
CC CONDUTER: Qa
CC CONDUTER: Qa
CC CONDUTER: CA
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77 YIKLKTAINIYIFNLALADALAISILPFQSAKYLMETWPFGELLCKAVLSIDYYNMFTSI 136
                                                                                                                                                                                       137 FILTMMSVDRYIAVCHPVKALDFRTPAKAKLINICIWVLASGVGVPIMVMAVTQPRDGA- 195
                                                                                                                                                                                                                                                                                          9
                                                                                                          Gaps
                                                                                                                                                 61 FILTHWAYDRYIAVCHPVKALDFRIPLKAKIINICIWLLSSSVGISAIVLGGIKVREDVD
                                                                                                                                                                                                                                        196 VV-CMLQFPSPSW-YWDIVTKICVFLFAFVVPILLIITVCYGLMLLRLRSVRLLSGSKEKD
                                                                                                                                                                                                                                                      4.
                                                                               Length 372;
                                                                             Score 1448; DB 2; Length 37:
Pred. No. 2.53e-115;
44; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: A NOVEL MAMMALIAN OPIOID TITLE OF INVENTION: RECEPTOR LIGAND AND USES NUMBER OF SEQUENCES: 16
ADDRESSEE: Klarquist Sparkman Campbell ADDRESSEE: Klarquist Sparkman Campbell ADDRESSEE: Leigh & Whinston LLP STREET: 121 S.W. Salmon, Suite 1600 CIIY: Portland
                                                                                                                                                                                                                                                                                                                                                                                                                             AA.
                                                                                                                                                                                                                                                                                                                                                                                                                             398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Burzow, James R.
APPLICANT: Grandy, David K.
APPLICANT: Civelli, Olivier
APPLICANT: Reinscheid, Rainer K.
APPLICANT: Ne. 583809hacker, Hans-Peter
APPLICANT: Nonsma, Frederick J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WP5.1 ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/514,451A
FILING DATE: 08/11/95
                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                         TOPOLOGY: linear
CE 372 AA; 40561 MW; 727422 CN;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/553,058
FILING DATE: 11/13/95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08514451A Patent No. 5837809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08514451A
 LENGTH: 372 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                               314 NPVLYAFLDENFKRCFRQLC 333
                                                                                                                                                                                                                                                                                                                                                             240 NPILYAFLDENFKRCFRDFC 259
             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy I
COMPUTER: IBM PC com
                                                                              Query Match
Best Local Similarity 68.8%;
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oregon
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US-08-514-451A-8
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                                                       SECUENCE
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Patent No. 5985001
GENERAL INFORMATION:
APPLICANT: EVANS, CHRISTOPHER J.
APPLICANT: EVERTH JR., DUANE E.
APPLICANT: EDWARDS, ROBERT H.
TITLE OF INVENTION: EXPRESSION CLONING OF A DELTA OPIOID
TITLE OF INVENTION: PHARMACEUTICALS
NUMBER OF SEQUENCES: 15
                                                                                                                                                           VV-CMLQFPSPSW-YWDTVTKICVFLFAFVVPILIITVCYGLMLLRLRSVRLLSGSKEKD 253
                                                                                                                                                                          77 YTKLKTATNIYIFNLALADALATSTLPFQSAKYLMETWPFGELLCKAVLSIDYYNMFTSI 136
                                                                                                          FILIMMSVDRYIAVCHPVKALDFRTPAKAKLINICIWVLASGVGVPIMVMAVTQPRDGA- 195
                                                                                                                         61 FILTHWAYDRYIAVCHPVKALDFRTPLKAKIINICIWLLSSSVGISAIVLGGTKVREDVD 120
                                                                       1 YIKMKTAINIYIFNLALADALVTITMPFQSIVYLMNSWPFGDVLCKIVISIDYNNFTSI 60
                              Gaps
                                                                                                                                                                                                                 254 RSLRRITRMVLVVVGAFVVCWAPIHIFVIVWTLVDINRRDPLVVAALHLCIALGYANSSL
                              4;
Score 1448; DB 2; Length 372;
Pred. No. 2.53e-115;
44; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THE PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRAIN APPLICATION DATA:
APPLICATION NUMBER: US/08/411,859
                                                                                                                                                                                                                                                                                                                                                 372 AA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/929,200
FILING DATE: 13.AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/08411859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36,856
REFERENCE/DOCKET NUMBER: 2200
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-0792
TELERAX: 706141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                314 NPVLYAFLDENFKRCFRQLC 333
 Query Match 65.0%;
Best Local Similarity 68.8%;
Matches 179; Conservative
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ZIP: 94304-1018
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ID US-08-411-859-10
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Search completed: Thu Feb 17 11:17:26 2000 Job time: 9 secs.
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                                                                                                                                                                                                                                                                                                       273 RNLRRITRMVLVVVAVTIVCWTPIHIYVIIKALITIPETTFQTVSWHFCIALGYTMSCLM 332
                                                                                                                                                                                                                                                 156 FTLCTMSVDRYIAVCHPVKALDFRTPRNAKIVNVCNWILSSAIGLPVMFMATTKYRQG-S 214
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08454549
Patent No. 5865324
GENERAL INFORMATION:
APPLICANT: BEPLIER, C. Mark
APPLICANT: OZENBERGER, Bradley A.
APPLICANT: HILMES, Jeffrey D.
APPLICANT: HILMES, Jeffrey D.
APPLICANT: HILMES, Jeffrey D.
TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
TITLE OF INVENTION: TO OPIOID RECEPTORS
                                                                                                                                                                                    4;
                                                                                                                                                             Length 398;
                                                                                                                                                                                                                                                                                                                                                                                            333 PVLYAFLDKMTKRCTREFCIPTSSTIEQQNSTRVRQNTREHPSTANTVD 381
                                                                                                                                                             Score 1426; DB 2; Length 391
Pred. No. 2.28e-113;
46; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
CONFUTER: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                330 AA
                     899-45995/WDN
NAME: William D. NO. 5837809nan, M.D. REGISTRATION NUMBER: 30,878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/454,549 FILING DATE: 30-MAY-1995
                                                                                                                              DESCRIPTION: peptide
SEQUENCE 398 AA; 44467 MW; 888796 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Darby & Darby, P.C. 805 Third Avenue
                  REPERENCE/DOCKET NUMBER: 899-
TELECOMMUNICATION INFORMATION:
TELEFONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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                                                                                      : 398 amino acids
amino acid
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Local Similarity 62.6%;
es 181; Conservative
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CORRESPONDENCE ADDRESS:
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STATE: New York
                                                                                              TYPE: amino de TOPOLOGY: lir
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US-08-454-549-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 GSTSHSTAALSSYYECIALGYINSSLNPILYAFLDENFKRCFRDFCFPLKMXMERXSISR 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 62.1%; Score 1385; DB 2; Length 330; Best Local Similarity 87.6%; Pred. No. 9.99e-110; Matches 177; Conservative 14; Mismatches 10; Indels
                                                 KEGISTRATION NUMBER: 23,148
REPERENCE/DOCKET NUMBER: 0646/1A818-US5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEPA: 22,237
TELEFAX: 22,227
TELEFAX: 22,227
                                                                                                                                                                                                                                                                                                                                                                                                        IISM: Rat
330 AA; 36851 MW; 611728 CN;
                                                                                                                                                                                                                                                                                                       STRANDEDNESS: not relevant TOPOLOGY: not relevant
                                          NAME: Robinson, Joseph R. REGISTRATION NUMBER: 33,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 VRNTVQDPASMRDVGGM-NKPV 330
              ATTORNEY/AGENT INFORMATION:
NAME: Robinson, Joseph R
                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 5 SEQUENCE CHARACTERISTICS: LENGTH: 330 amino acids ITPE: amino acids
                                                                                                                                                                                                                                                                                                                                TOPOLOGY: not releva:
MOLECULE TYPE: protein
ORIGINAL SOURCE:
CLASSIFICATION:
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Feb 17 11:15:32 2000; MasPar time 15.81 Seconds 747.854 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-455-683-12 (1-295) from USO8455683.pep 2229 1 YTKMKTATNIYIENLALADA......NTVQDPAYLREIDGMANKPV 295 Title: Description: Perfect Score:

Sequence:

Scoring table:

PAM 150 Gap 11

122810 segs, 40068593 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

Mean 47.358; Variance 110.368; scale 0.429 pir60 1:pir1 2:pir2 3:pir3 4:pir4 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Pred. No.	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	8.97e-243	1.36e-242	.06e-2	.75e-24	.75e-24	.45e-23	.65e-23	5e-23	.28e-23	.90e-22	.86e-21	.27e-21	e - 21	.19e-20	.66e-11	.66e-1	6e-11
	Description	kappa opicid receptor	opioid receptor kappa	kappa opioid receptor	opioid		pioido.	mu opioid receptor -	delta opicid receptor	opiate receptor mu -	opioid receptor mu va	mu-opioid receptor	mu opicid receptor -	.π	Ö	æ	delta opioid receptor	G protein-coupled rec	opioid receptor homol	K3 opiate receptor -	orphan opioid recepto	somatostatin receptor	somatostatin receptor	somatostatin receptor
SUMMAKLES	Q H	233	00	52	22	514	JC2434	A57510	JE0087	I56553	865693	156517	I56504	I38657	I38532	S34592	B48227	I56520	JC2421	I49022	S43087	53	C41795	79
	DB	7	N	N	N	7	7	7	N	7	7	~	N	7	7	7	7	7	7	7	7	7	N	7
	Length	380	380	380	380	380	380	398	373	400	392	398	398	372	372	372	372	367	367	367	370	391	391	391
ж	Query Match	98.3	98.3	8.96	95.8	92.6	94.8	68.4	68.3	68.3	68.2	68.2	67.5	65.4	65.4	65.1	65.0	60.3	60.3	60.2	$\sigma$	~	37.2	_
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	The complete receptor - by the sapient sequence_receptor - conson, p. S. Conson	ansmemb ansmemb ansmemb ansmemb ansmemb ansmemb ansmemb lecula Score Fred. 1; M TITMPFQ
$\alpha$	#typp #typp #see 55 #see 5354 5354 Ba iophy 43383 43383 ##lal place ##lal place adynoi 50144 minar 113611 11361	DALL S. # # The truck of the tr
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90000000000000000000000000000000000000	RESULT ENTRE TITLE ORGANISM DATE DATE ACCESSION REFERENCE # author # fille # # in # # in # in # in # in # in # in	60-6 133-1 1377 228 278 311- SUMMARY Query Best Matci

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326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 FILTMMSVDRYIAVCHPVKALDFRTPLKAKIINICIWLLSSSVGISAIVLGGTKVREDVD 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 VIECSLQFPDDDYSWWDLFMKICVFIFAFVIPVLIIIVCYTLMILRLKSVRLLSGSREKD 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YTKWKTATNIXIFNLALADALVITTMPFQSTVYLMNSWPFGDVLCKIVISIDYINNFTSI 60
                                                                                                                                                                                                                                                                                               157005 #type complete opioid receptor kappa-l - human #formal_name Homo sapiens #common_name man 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Aug-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A55259 #type complete
Kappa opioid receptor - guinea pig
dynozphin receptor
#formal_name Cavia porcellus #common_name guinea pig
06_reb-1995 #sequence_revision 06-reb-1995 #text_change
A55259
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                    181 XNLRRITRLVLVVVAVFVVCWIPIHIFILVEALGSTSHSTAALSSYFCIALGYTNSSLN
FILIMMSVDRYIAVCHPVKALDFRTPLKAKIINICIWLLSSSVGISAIVLGGTKVREDVD
                                                                                                                                          RNLRRITRLVLVVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLN
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                                                                      VIECSLQFPDDDYSWWDLFMKICVFIFAFVIPVLIIIVCYTLMILRLKSVRLLSGSREKD
                                                                                                     121 VIECCLQFPDDDYSWWDLFMKICVFIFAFVIPVLIIIVCYTLMILRLKXVRLLSGSREKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##cross-references GDB:132651; OMIM:165196
#map_position 8q11.2-8q11.2
#MARY #length 380 #molecular-weight 42645 #checksum 8302
                                                                                                                                                                                                            PILYAFIDENFKRCFRDFCFFLKMRMERQSTSRVRNTVQDPAYLRDIDGM-NKPV 380
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                                                                                                                                                                                                                                Length 380;
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Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhu, J.; Chen, C.; Xue, J.
Life Sci. (1995) 56:201-207
Cloning of a human .kappa. opioid
I57005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##cross-references GB:L37362;
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ilarity 97.6%;
Conservative
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##molecule_type mRNA
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Best Local Similarity
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ALTERNATE_NAMES
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ORGANISM
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Proc. Natl. Acad. Sci. U.S.A. (1993) 90:6736-6740
Cloning and functional comparison of kappa and delta opioid receptors from mouse brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This receptor exists in different areas of the central and peripheral nervous systems, and mediates many physiological and pharmacological effects of opiates and opioid compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu, H.C.; Lu, S.; Augustin, L.B.; Felsheim, R.F.; Chen, H.C.; Loh, H.H.; Wei, L.N.
Blochem. Biophys. Res. Commun. (1995) 209:639-647
Cloning and promoter mapping of mouse kappa opioid receptor
              Xie, G.; Meng, F.; Mansour, A.; Thompson, R.C.; Hoversten, M.T.; Goldstein, A.; Watson, S.J.; Akil, H. Proc. Natl. Acad. Sci. U.S.A. (1994) 91:3779-3783 Primary structure and functional expression of a guinea pi kappa opioid (dynorphin) receptor.
                                                                                                                                                                                                                                                                                                                                                                     87 YTKMKTATNIYIENLALADALVTTTMPFOSTVXLMNSWPFGDVLCKIVISIDXYNMFTSI 146
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Kappa opioid receptor 1 - mouse
*formal_name Mus musoulus #common_name house mouse
26-May-1994 *sequence_revision 26-May-1994 #text_change
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#length 380 *molecular-weight 42736 *checksum 7081
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##cross-references GB:U04092; NID:g476106; PID:g476107
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Pred. No. 0.00e+00; ?
10; Mismatches 5;
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Biochem. J. (1993) 295:625-628
Wolecular cloning of a rat kappa opioid receptor reveals
sequence similarities to the mu and delta opioid receptors.
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Li, S.; Zhu, J.; Chen, C.; Chen, Y.W.; Deriel, J.X.; Ashby,
                                                                                                                                         87 YTKMKTAINIYIFNLALADALVTTIMPFQSAVYLMNSWPFGDVLCKIVISIDYYNMFTSI 146
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##cross-references GB:D16534; NID:g409390; PID:d1004487; PID:g415310
                                                                                                                                                           brain; G protein-coupled receptor; glycoprotein; opioid
  peptide; phosphoprotein; transmembrane protein
  #length 380 #molecular-weight 42652 #checksum 9937
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#authors Nishi, M.; Takeshima, H.; Fukuda, K.; Kato, S.; Mori, #journal FEBS Lett. (1993) 330:77-80
#title cDNA cloning and pharmacological characterization of cploid receptor with high affinities for kappa-subtype-selective ligands.
#cross-references MUID:93380575
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##molecule_type mRNA
##residues 1-380 ##label CHE
##cross-references GB:L22001; NID:g409235; PID:g409237
ENCE S36102
                                                                   Score 2136; DB 2; Leg
Pred. No. 0.00e+00;
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#cross-references MUID:93374033
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larity 92.9%;
Conservative
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*#molecule_type mRNA
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Proc. Natl. Acad. Sci. U.S.A. (1993) 90:9954-9958
Cloning and pharmacological characterization of a rat kappa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. (1994) 205:1353-1357
Structure and chromosomal mapping of genes for the mouse
kappa-opioid receptor and an opioid receptor homologue
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#formal_name Mus musculus #common_name house mouse
21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change
                                              a rat kappa opioid
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##residues 1-380 ##label RES
##cross-references EMBL:U00442; NID:9403486; PID:9403487
ROS G protein-coupled receptor; transmembrane protein
XX #length 380 #molecular-weight 42688 #checksum 9972
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#length 380 #molecular-weight 42630
B.; Liu-Chen, L.Y.
Biochem. J. (1993) 295:629-633
Molecular cloning and expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2132; DB 2;
Pred. No. 0.00e+00;
13; Mismatches 8;
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Best Local Similarity 92.5%;
Matches 273; Conservative
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92.58;
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#introns 86/2; 204/1
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##cross-references EMBL:U26915. NID:91055230; PID:91055231
##cross-references EMBL:U26915. NID:91055230; PID:91055231
##note the nucleotide sequence was submitted to the EMBL Data
##note Library. November 1995
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Magendzo, K.; Newman, D.; Tran, T.H.; Lee, D.S.; Wen, C.;
Xia, Y.R.; Lusis, A.J.; Evans, C.J.
J. Biol. Chem. (1995) 270:15877-15883
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Min, B.H.; Augustin, L.B.; Felsheim, R.F.; Fuchs, J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #formal_name Mus musculus #common_name house mouse 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 07-Nov-1997
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                                                                  YTKMKTATNIYIFNLALADALVITTMPPQSTVYLANSWPFGDVLCKIVISIDYNNFTSI
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95/2; 213/1; 386/3
alternative splicing; G protein-coupled receptor;
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##residues 1-398 ##label RES
##cross-references EMBL:U10561; NID:g555696; PID:g565069
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Genomic structure analysis of
opioid receptor gene.
ness MUID:94377496
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#cross-references MUID:95377399
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mu opioid receptor - mouse
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Garcia-Isidoro, M.; Rodriguez, R.E. Blochem. Blophys. Res. Commun. (1998) 245:544-548 Cloning, molecular cheralization, and distribution of a gene homologous to delta opioid receptor from zebrafish (Danio
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##cross-references EMBL:AJ001596; NID:g2739230; PID:e1217996;
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Pred. No. 1.36e-242;
52; Mismatches 40;
Score 1524; DB 2; ]
Pred. No. 8.97e-243;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors Bare, L.A.; Mansson, E.; Yang, D.
#journal FEBS Lett. (1994) 354:213-216
#title Expression of two variants of the human mu opioid receptor mRNA in SK.N-SH cells and human brain.
#cross-references MUID:95046336
                                                                                                                                                                                                                                CESSIONS I56553, A38991, S41075; S51215

#authors Mestek, A.; Huxley, J.H.; Bye, L.S.; Campbell, A.D.; Chen, Y.; Tian, M.; Liu, J.; Schulman, H.; Yu, L.
#journal J. Neurosci. (1995) 15:2396-2406

#title The human mu opicid receptor: modulation of functional desensitization by calcium/calmodulin-dependent protein kinase and protein kinase C.
#cross_references_MUID:95198115
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MOR1 protein; opioid receptor mu

#formal_name Homo sapiens #common_name man

02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change

21-Nov-1998
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##cross-references GB:L25119; NID:g452072; PID:g452073
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##cross-references GB:L29301; NID:q459831; PID:q459832
                      240 NPILYAFLDENFKRCFRDFCFPLKMXMERXSTSRVRNTVQDP 281
317 NPVLYAFLDENFKRCFRDFCLPFRTRADQSNLNRARNATREP
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Griffin, C.A.; Uhl, G.R.
submitted to GenBank, August 1994
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#map_position 6q24-6q25
KEYWORDS G protein-coupled receptor; qlv
                                                                                                                      #type complete
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##molecule_type mRNA
#*residues 387-460 ##label BAR
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FESS Lett. (1994) 354:213-216
Expression of two variants of the human mu opioid receptor
mRNA. in SK-N-SH cells and human brain.
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opioid receptor mu variant MORIA - human
#formal_name Homo sapiens #common_name man
12.7u1-1996 #sequence_revision 26.7u1-1996 #text_change
10.5p-1997; S51216
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      #checksum 3741
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##residues 387-392 ##label BAW
RY #length 392 #molecular-weight 43939 #checksum 6977
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submitted to the EMBL Data Library, July 1994
Expression of two variants of the human mu opioid
                                                 Length 400;
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##cross-references EMBL:U12569; NID:g607911; PID:g607912
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*length 400 #molecular-weight 44779
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#journal Biochem. Biophys. Res. Commun. (1995) 209:563-574
#title complementary DNA cloning of a mu-opioid receptor from rat
periteneal macrophages.
#cross-references MUID:95251654
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FEBS Lett. (1993) 327:311-314
Primary structures and expression from cDNAs of rat opioid
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                                                                                                                   mu-opioid receptor - rat
#formal_name Rattus norvegicus #common_name Norway rat
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
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J. Biol. Chem. (1993) 268:26447-26451
Purification and partial amino acid sequence of a
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                                                                                                                                                                                                                                                                                                                                                     ##residues 1-398 ##label RES
##cross-references EMBL:U02083; NID:g403573; PID:g403574
NCE 157951
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O.K.; Kelly, M.J.; Grandy, D.K.
J. Neurochem. (1995) 64:14-24
Characterization and distribution of a
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#accession S34593
335 PVLYAFLDENFKRCFREFCIPISSNIEQQNSTRIRQNTRD
                 receptor from rat brain. #cross-references MUID:94075333
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                                                                                                       #type complete
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##molecule_type protein
##residues 272-291 ##label EPP
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ANISM #formal_name Rattus norvegicus #common_name Norway rat
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
26-Jul-1996 #correction 26-Jul-1996 #text_change
156504 #authors Is6504
#authors Zastawny R.L.; George, S.R.; Nguyen, T.; Cheng, R.; Isatsos,
#journal J. Neurochem. (1994) 62:2099-2105
#title Cloning, characterization, and distribution of a mu-opicid
#cross-references MUID:94246380
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#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:10230-10234 #title Mu opiate receptor: cDNA cloning and expression. #cross-references MUID:94052137 #accession A48799
                                                                                                                                                                                                                                               #authors Thompson, R.C.; Mansour, A.; Akil, H.; Watson, S.J.
#journal Neuron (1993) 11:903-913
#title Cloning and pharmacological characterization of a ri
popioid receptor.
#cross-references MUID:94059560
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Pred. No. 2.45e-239;
45; Mismatches 50; Indels
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                                                                                                                                                                                                                                                                                                                                                                                 ##status preliminary; translated from GB/EMBL/DDBJ
##molemary mRNA
                                                                                                                          preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1520; DB 2; Length 39
Pred. No. 4.75e-242;
46; Mismatches 49; Indels
                                                                                                                                             ##residues 1-244,'V',246-398 ##label WAN
##cross-references GB:L20684; NID:G409149; PID:G409150
**NCE 158154
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Best Local Similarity 65.7%;
Matches 190; Conservative
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Best Local Similarity 65.7%;
Matches 190; Conservative
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                                                                               FILCIMSVDRYIAVCHPVKALDFRIPRNAKIVNVCNWILSSAIGLPVWFWATTKYRQG-S 214
                                                                                                                         -IDCTLIFSHPIW-YWENLLKICVGIFAFIMPVLIIIVCYGLMILRLKSVRMLSGSKEKD 272
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          YTKMKTAINIYIFNLALADALAISTLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSI 155
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                                   1 YTKWKTATNIYIENLALADALVTTMPFQSTVYIMNSWPFGDVLCKIVISIDXYNMFTSI 60
                                                                                                                                                                                                                                                                                                138657 #type complete
delta opiate receptor - human
#formal_name Homo sapiens #common_name man
06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
06-Sep-1996
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##cross-references EMBL:U10504; NID:g501144; PID:g501145
##cross-references EMBL:U10504; NID:g501144; PID:g501145
XX #length 372 #molecular-weight 40368 #checksum 1688
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Pred. No. 7.65e-231;
43; Mismatches 33; Indels
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delta opioid receptor - human
#formal_name Homo sapiens #common_name man
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534592
Fukuda, K.; Kato, S.; Mori, K.; Nishi, M.; Takeshima, H.
FEBS Lett. (1993) 327:311-314
Primary structures and expression from CDNAs of rat opioid
                                                                                                                                                   Yamamura, H.I.
Life Sci. (1994) 54:PL463-PL469
Identification of a human delta opioid receptor: Cloning
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##molecule_type_mRNA
##residues 1372 ##label FUK
##cross-references GB:D16348; NID:g391864; PID:d1004367; PID:g391865
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29-May-1998 #sequence_revision 29-May-1998 #text_change
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#formal_name Rattus norvegicus #common_name Norway rat
10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change
29-Jan-1999
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                                                                                                     L.; Xiaoping, L.;
uby, V.J.; Roeske,
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##cross-references EMBL:U07882; NID:q497313; PID:q497314
##cross-references EMBL:U07882; NID:q497313; PID:q497314
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Pred. No. 7.65e-231;
43; Mismatches 33; Indels
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##cross-references EMBL:UO0475; NID:g403488; PID:g514211
                                                                                                     Knapp, R.J.; Malatynska, E.; Fang, L.;
M.; Santoro, G.; Varga, E.V.; Hruby,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Neurosci. Res. (1994) 27:714-719
Molecular cloning and expression of
receptor from rat brain.
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G protein-coupled receptor; transmembrane protein

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254 RSLRRITRMVLVVVGAFVVCWAPIHIFVIVWTLVDINRRDPLVVAALHLCIALGYANSSL 313
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Pred. No. 9.28e-230;
44; Mismatches 33; Indels 4; Gaps
#length 372 #molecular-weight 40449 #checksum 2221
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Search completed: Thu Feb 17 11:15:49 2000 Job time : 17 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Feb 17 11:16:07 2000; MasPar time 10.89 Seconds 766.047 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-455-683-12 (1-295) from USO8455683.pep 2229 1 XTKMKTATNIYIFNLALADA......NTVQDPAYLREIDGMMNKPV 295

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

77977 seqs, 28268293 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot37 1:swissprot Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 48.475; Variance 96.994; scale 0.500 Statistics:

## SUMMARIES

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IN RECEPT		22	нын	PROBABLE G PROTEIN-COU MU-TYPE OPIOID RECEPTO SOMATOSTATIN RECEPTOR SOMATOSTATIN RECEPTOR	GALANIN RECEPTOR TYPE GALANIN RECEPTOR TYPE GALANIN RECEPTOR TYPE GALANIN RECEPTOR TYPE	E G PROTEIN-C MOKINE RECEPT ANGIOTENSIN I
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4 10 00	2220	3888	38.84 48.44	, w w w c	2444 2010	44 45 5

## ALIGNMENTS

ALIGNMENTS	RESULT 1 ID OPRK_HUMAN STANDARD; PKT; 380 AA. AC P4.1145.		HOMO S EUKARN PRIMAT	ROUTE FROM N.A.  RC TISSUE-PLACENTA;  RA MEDLINE; 94338360.  RA MANSON E., BARE L.A., YANG D.;  RI "Isolation of a human kappa opioid receptor CDNA from placenta.";  RI BICCHEM. BIOPHYS. RES. COMMUN. 202:1431-1437(1994).		SEQUENCE FROM N.A. TISSUE-BRAIN, MEDLINE; 95174504. ZHU J., CHEN C., XUNE JC., KUNAPULI S. "Cloning of a human kappa opioid receptings of 50. 56:201-207(1995)!- FUNCTION: INHIBIT'S NEUROTRANSMITTER ION CURRENTS AND INCREASING POTASSIF FOR DYNORHINS. MAY PLAY A ROLE IN AUTONOMIC AND NEUROENDOCRINE FUNCTI -!- SUBCELLULAR LOCATION: INTEGRAL MEMB	This SWISS-PROT between the Sw the European Bi use by non-pr modified and th
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; HYSTRICOGNATHI; CAVILDAE; CAVIA.
                                                                                                                                                                                                                                                                                                          Length 380;
                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                  PEAM; PF00001; 7tm_1; 1.
G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
                                                                                                                                                                                                                    6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                  2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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                                                                                                                    PALMITATE.
EXTRACELLULAR (POTENTIAL).
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1980629E CRC32;
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                   1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                    BY SIMILARITY.
PALMITATE (POTENTIAL).
                                                                                                                                                                                                                                                                                                          Score 2192; DB 1;
Pred. No. 0.00e+00;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REL. 31, CREATED)
(REL. 31, LAST SEQUENCE UPDATE)
(REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               380 AA
                                                                                                                                                                                 4 (POTENTIAL).
                                                                                                                                                                                                    5 (POTENTIAL).
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                                                                                            PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
                                                                                                                                                                                                                                                                             POTENTIAL
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OPR1144;
01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 35, LAST ANNOFATION
KAPPA-TYPE OPIOID RECEPTOR (KOR-1).
                                                                                                                                                                                                                                                                                           42659 MW;
                                                                                                                                                                                                                                                                                                          98.3%;
Local Similarity 97.6%;
les 288; Conservative
                         EMBL, U11053; G532060; -. EMBL, U17298; G596070; -. EMBL; L37362; G722618; -. PIR, JC2338; JC2338.
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1117
1132
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1173
222
247
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299
311
333
380
210
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                                                            GCRDB; GCR_1819;
                                                                                     MIM; 165196;
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TRANSMEM
DOMAIN
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CARBOHYD
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TRANSMEM
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                                                                    GCRDB;
GCRDB;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in EO way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                        XIE G.X., MENG F., MANSOUR A., THOMPSON R.C., HOVERSTEN M.T.,
GOLDSTEIN A., WATSON S.J., AKIL H.;
GOLDSTEIN A., WATSON S.J., AKIL H.;
"Primary structure and functional expression of a guinea pig kappa
opioid (dynorphin) receptor.";
PROC. NATL. ACAD. SCI. U.S.A. 91:3779-3783(1994).
-!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSEL AND REGULATION OF
AUTONOMIC AND NEUROENDOCKINE FUNCTIONS.
                                                                                                                                                                                                                                                                                         -i-SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
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                                                                     THOMPSON R.C., HOVERSTEN M.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
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BY SIMILARITY.
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PALMITATE (POTENTIAL).
POTENTIAL.
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Pred. No. 0.00e+00;
10; Mismatches 5;
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F9F34C4C CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCRDB; GCR_0991; -.
PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PALMITATE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION; LIPOPROTEIN;
SEQUENCE FROM N.A.
STRAIN=HARTLEY; IISSUE=BRAIN;
MEDLINE; 94224825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00001; 7tm_1; 1.
G-PROTEIN COUPLED RECEPTOR;
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Conservative
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39
380 AA;
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155
174
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87 YTKWKTAINIYIFNLALADALVTTTMPFQSAVYLMNSWPFGDVLCKIVISIDYYNMFTSI 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHEN Y., MESTER A., LIU J., YU L.; "MOlecular cloning of a rat kappa opioid receptor reveals sequence similarities to the mu and delta opioid receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNLRRITKLVLVVVVAVFIICWTPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSLN
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EUKARXOIA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RAITUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2136; DB 1; Length 380; Pred. No. 0.00e+00;
                          GCRDB; GCR_2355; --
MGD; MG197439; OPRK1.
PROSITE; PSG0237; GPROTEIN_RECEPTOR; 1.
PRAM; PF00001; 7tm_1; 1.
G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; PHOSPHORYLATION; LIPOPROTEIN; PALMITARIA.
                                                                                                                                  EXTRACELLULAR (POTENTIAL).

1 (POTENTIAL).
                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                    4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                  5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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F -> V (IN REF. 2 AND 3).
C6F33212 CRC32;
                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                     7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
PALMITATE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
KAPPA-TYPE OPICID RECEPTOR (KOR-1).
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01-FEB-1994 (REL. 28, LAST SEO)
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42652
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               GCRDB; GCR_1933; -.
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380 AA;
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Best Local Similarity
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MEDLINE; 94059008.
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223
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DISULFID
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CONFLICT
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P34975;
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                                                                                                                              DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning and promoter mapping of mouse kappa opicid receptor gene."; BIOCHEM, BIOPHYS. RES. COMMUN. 209:639-647(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. NEURCHMUTNOL. 62:113-117(1995).

1. FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM ON CURRENTS AND INCREASING POTASSIUM ION CONDUCIANCE. RECEPTOR FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF AUTONOMIC AND NEUROBENDORINE FUNCTIONS.

1. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

1. ILSSUE SPECIFICITY: BRAIN (NEOCORTEX, HIPPOCAMPUS, ANYGDALA, MEDIAL HABENULA, HYPOTHALAMUS, LOCUS CERULEUS, AND PARABRACHIAL
                                                                                                                                                                                                                                                                  TISSUE-BRAIN;
BEDLINE, 93342064.
YASUDA K., RAXNOR K., KONG H., BREDER C.D., TAKEDA J., REISINE T.,
BELL G.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE, 92100967.
NISHI M., TAKESHIMA H., MORI M., NAKAGAWARA K.I., TAKEUCHI T.;
"Structure and chromosomal mapping of genes for the mouse kappa-opioid receptor and an opioid receptor homologue (MOR-C).";
BIOCHEM. BIOPHYS. RES. COMMUN. 205:1353-1357(1994).
241 PILYAFLDENFKRCFRDFCFPLKMXMERXSTSRVRNTVQDPAYLREIDGMMNKPV 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 96084989.

BELKOWSKI S.M., ZHU J., LIU-CHEN L.Y., EISENSTEIN T.K.,
ADLER M.W., ROGERS T.J.;
"Sequence of kappa-opicid receptor cDNA in the RI.1 thymoma cell
                                                                                                                                                                                                         MAMMALIA; EUTHERIA;
MUS.
                                                                                                                                                                                                                                                                                                                                 "Cloning and functional comparison of kappa and delta opioid receptors from mouse brain.";
PROC. NATL. ACAD. SCI. U.S.A. 90:6736-6740(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE, 95251663.
LIU H.C., LU S., AUGUSTIN L.B., FELSHEIM R.F., CHEN H.C.,
LOH H.H., WEI L.N.;
                                                                                               01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDAIE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
KAPPA-TYPE OPIOID RECEPTOR (KOR-1) (MSL-1).
                                                                     380 AA
                                                                                                                                                                                 MUS MUSCULUS (MOUSE),
EUKARYOTA, METAZOA, CHORDAIA, VERTEBRATA,
RODENTIA, SCIUROGNATHI, MURIDAE, MURINAE,
                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, L11065; G348249; --
EMBL, D31665; G808876; --
EMBL, D31664; G808876; --
EMBL, D31664; G808876; JOINED.
EMBL, S77868; G998532; --
EMBL, S77869; G998532; JOINED.
EMBL, S77869; G998532; JOINED.
EMBL, S8111; E257489; --
PIR, A48227; GGCRDB; GCR_0635; --
                                                                   STANDARD;
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                LT 3
OPRK_MOUSE
P33534;
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7

Gaps

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7; Indels

380

AA

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ROSSI G.C., PAN Y.X., BROWN G.P., PASTERNAK G.W.;
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LIPOPROTEIN;
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Local Similarity 92.5%;
nes 273; Conservative
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MEDLINE; 95377399
      PHOSPHORYLATION;
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TRANSMEM
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TRANSMEM
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                                                                                                                                                                     "Cloning and expression of a CDNA for the rat kappa-opioid receptor.";
FEBS LETT. 329:291-295(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NISHI M., TAKESHIMA H., FUKUDA K., KATO S., MORI K.; "CDNa cloning and pharmacological characterization of an opioid receptor with high affinities for kappa-subtype-selective ligands."; FEBS LETT. 330:77-80(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAROVLEY A.G., KRUEGER K.E., FADEN A.I.;

YAKOVLEV A.G. KRUEGER K.E., FADEN A.I.;

SIGNICTURE and expression of a rat kappa opioid receptor gene.";

J. BIOL. CHEM. 270:6421-6424(1995).

I. BIOL. CHEM. 270:6411-1995).

I. FUNCITION: INHIBITS NEUDOTRANNAITHER RELEASE BY REDUCING CALCIUM ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR FOR DYNORPHINS. MAY PLAX A ROLE IN AROGRAL AND REGULATION OF AUTONOMIC AND NEUROBNOCRINE FUNCITIONS.

I. SUBCELLULAR LOCATION: INTEGRAL MEMBERANE PROTEIN.

I. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE: 94052210.
MENG F., XIE G.-X., THOMPSON R.C., MANSOUR A., GOLDSTEIN A.,
WATSON S.J., AKIL H.;
"Cloning and pharmacological characterization of a rat kappa opioid
                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning and expression of a rat kappa opioid receptor.";
BIOCHEM. J. 295:629-633(1993).
                                                                                                                     MINAMI M., TOYA T., KAIAO Y., MAEKAWA K., NAKAMURA S., ONOGI T.,
KANEKO S., SATOH M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCRDB; GCR_0724; -.
GCRDB; GCR_0790; -.
GCRDB; GCR_1282; -.
GCRDB; GCR_1282; -.
GCRDB; GCR_1282; -.
FROSTIR; PSO0237; -.
FROSTIR; PSO0137; Tm_1; 1.
FRAM: PFO001; 7tm_1; 1.
G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLXCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                        MEDLINE; 94059009.
LI S., ZHU J., CHEN C., CHEN Y.-W., DERIEL J.K., ASHBY B.
LIU-CHEN L.-Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROC. NATL. ACAD. SCI. U.S.A. 90:9954-9958(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-SPRAGUE-DAWLEY; TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                      STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
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                     BIOCHEM. J. 295:625-628(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=WISTAR, TISSUE=BRAIN;
MEDLINE; 93380575.
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MEDLINE; 95204422.
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PIR; S3825; S38825.
GCRDB; GCR_0636: -
                                                   [2]
SEQUENCE FROM N.A.
WPDT.INE; 93374033.
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receptor

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[1]
SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE=LIVER;
MEDLINE; 94377496.
MIN B.H., AUGUSTIN L.B., FELSHEIM R.F., FUCHS J.A., LOH H.H.;
MENOMIC structure analysis of promoter sequence of a mouse mu opicid
"Genomic structure analysis of promoter."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 YIKMKTATNIYIENLALADALVTTTMPFQSAVYLMNSWPFGDVLCKIVISIDYYNMFTSI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIECSLQFPDDEXSWWDLFMKICVFVFAFVIPVLIIIVCYTLMILRLKSVRLLSGSREKD 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
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                                                                                                   3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELULAR.
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                                                              2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                      7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
                     1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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V -> L (IN REF. 2).

C -> Y (IN REF. 3).

4; EE858A46 CRC32;
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Pred. No. 0.00e+00;
13; Mismatches 8;
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0P42866; Q60768;
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 36, LAST SEQUENCE UPDATE)
01-UL-1998 (REL. 36, LAST ANNOTATION UPDATE)
MU-TYPE OPICID RECEPTOR (MOR-1).
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                                                                                                                "Characterization of the murine mu opioid receptor gene.";
J. BIOL. CHEM. 270:15877-15883(1995).
-!- FUNCTION: INFIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
                                                                                                                                                   FOR BEATA-ENDORPHIN.
-!- SUMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-!- SIMILARITY: BELONGS TO FAMILY 1.
"Antisense mapping the MOR-1 opioid receptor: evidence for alternative splicing and a novel morphine-6 beta-glucuronide
                                                                                  KAUFMAN D.L., KEITH D.E., ANTON B., TIAN J., MAGENDZO K., NEWMAN D., TRAN T., LEE D.S., WEN C., XIA Y., LUSIS A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUGAR (POTENTIAL).
3 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                            EMBL; O15300, OUT.), GCRDB; GCR_1312; -... GCRDB; GCR_1699; -. GCRDB; GCR_1707; -.. MGD; MGI:97441; OPRM.
PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
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POTENTIAL.
POTENTIAL.
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EMBL; U10558; G565069; JOINED.
EMBL; U10559; G565069; JOINED.
EMBL; U10569; G555069; JOINED.
EMBL; U26915; G105531; --
EMBL; U19380; G885865; --
                               FEBS LETT. 369:192-196(1995)
                                                SEQUENCE FROM N.A. STRAIN=BALB/C; TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44421 MW;
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143
163
193
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257
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                                                    SEQUENCE STRAIN STRAIN 95318184
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22
398 AA;
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214
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                                                                                                                                                                                                                                                                                   FUKUDA K., KATO S., MORI K., NISHI M., TAKESHIMA H.;
"Primary structures and expression from CDNAs of rat opioid receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=BRAIN;
MEDITUR; 93341493.
(TEN Y., MESTEK A., LIU J., HURLEY J.A., YU L.;
"Molecular cloning and functional expression of a mu-opioid receptor from rat brain.";
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MEDLINE: 94246380.
ZASTANNY R.L., GEORGE S.R., NGOYEN T., CHENG R., TSATSOS J.,
BRIONES-URBINA R., O'DOWD B.F.;
"Cloning, characterization, and distribution of a mu-opioid receptor in rat brain.";
J. NEUROCHEM. 62:2099-2105(1994).
FILCIMSVDRYIAVCHPVKALDFRIPRNAKIVNVCNWILSSAIGLPVMFMAITKYRQG-S
                                                                                                                        -IDCTLTFSHPTW-YWENTLKICVFIFAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKD
                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; IISSUE-OLFACTORY BULB;
MEDLINE; 94059560.
THOMPSON R.C., MANSOUR A., AKIL H., WATSON S.J.;
"Cloning and pharmacological characterization of a rat mu opioid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UHL G.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNAIHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LT 6
OPRM_RAT
1918 AA.
1918 AA.
1918 AA.
1918 AA.
1918 AA.
1918 AEL. 28, CREAIED,
101-FEB-1994 (REL. 28, CREAIED)
101-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
115-UTL-1998 (REL. 36, LAST ANNOTATION UPDATE)
116-UTLPE OPPOID RECEPTOR (MOR-1) (OPIOID RECEPTOR B) (MUORI).
                                                                                                                                                                                                                                                                                                                                                                                      381
                                                                                                                                                                                                                                                                                                                                                                   333 PVLYAFLDENFKRCFREFCIPISSTIEQONSARIRQNTREHPSTANIVD
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 94052137.
WANG J.-B., IMAI Y., EPLER M.C., GREGOR P., SPIVAK C., "Mu opiate receptor: cDNA cloning and expression.";
PROC. NATL. ACAD. SCI. U.S.A. 90:10230-10234 (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BUNZOW J.R., GRANDY D.K., KELLY M.;
SUBMITTED (SEP-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          delta- and mu-subtypes."; FEBS LETT. 327:311-314(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOL. PHARMACOL. 44:8-12(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RATIUS NORVEGICUS (RAI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor.";
NEURON 11:903-913(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 93351652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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4;

Gaps

4

Length 398;

Score 1524; DB 1; Length 398 Pred. No. 2.17e-282; 47; Mismatches 48; Indels

68.48; 65.78; Conservative

Best Local Similarity Matches 190; Conser

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Query Match

96 YIKMKIAINIYIFNLALADALATSILPFQSVNYLMGTWPFGNILCKIVISIDYYNMFTSI 155

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CONFLICT
CONFLICT
CONFLICT
SEQUENCE
           CARBOHYD
                      CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                               SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: BRAIN. IS EXPRESSED IN THE CEREBRAL CORTEX,
CAUDATE PUTAMEN, NUCLEIS ACCUMBENS, SEPTAL NUCLEI, THALAMUS,
HIPPOCAMPUS, AND HABBULA. NOT DETECTED IN CEREBELLUM.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                            MEDLINE; 95172221.
ZIMPRICH A., SIMON T., HOLLT V.;
"Cloning and expression of an isoform of the rat mu opioid receptor (rMORIE) which differs in agonist induced desensitization from
                                                                                                                                                                             rmorl.";
FEBS LETT. 359:142-146(1995).
-!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
-!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
FOR UTRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR FOR BETA-ENDORPHIN.
                                                              Complementary DNA cloning of a mu-opioid receptor from rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).

(VOTENTIAL).

(VTODLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
PPAM; PF00001; 7tm_1; 1.
G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; PHOSPHORYLATION; LIPOPROTEIN; PLAMITATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLESMIC (POTENTIAL).
BY SIMILARITY.
PALMITATE (POTENTIAL).
POTENTIAL.
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CYTOPLASMIC (POTENTIAL).
                                           MEDLINE; 95251654.
SEDQI M., ROY S., RAMAKRISHNAN S., ELDE R., LOH H.H.;
                                                                         peritoneal macrophages.";
BIOCHEM. BIOPHYS. RES. COMMUN. 209:563-574(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 (POTENTIAL).
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                                                                                                                SEQUENCE OF 356-391 FROM N.A.
        [7]
SEQUENCE OF 101-340 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D16349; G391867; --
EMBL; L20684; G409150; --
EMBL; L13069; G348251; --
EMBL; U20203; G403574; --
EMBL; U22455; G437672; --
EMBL; G3544; G1017732; --
EMBL; S77863; E199500; --
EMBL; S77863; E199500; --
EMBL; S75669; G861432; --
PIR; S34593; S34593; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IISSUE=MACROPHAGE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
TRANSMEM
DOMAIN
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DISULFID
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TRANSMEM
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181 XNLRRITRLVLVVVVAVFVVCWTPIHLFILVEALGSTSHSTAALSSYYFCIALGYTNSSLN 240
                                                                                                                                                                                                                                                                                                                                96 YIKMKTAINIYIENLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDXYNMFTSI 155
                                                                                                                                                                                                                                                  156 FILCIMSVDRYIAVCHPVKALDFRIPRNAKIVNVCNWILSSAIGLFVMFMAITKYRQG-S 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIJER; 95046336.

BARE L.A., MANSSON E., YANG D.;

SEN-N-SH cells and human brain.";

SEN-N-SH cells and human brain.";

IN CURPLIA SA: 213-216(1994).

IN CURPLIA INITELTS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM

ION CURPLIA NO INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR

FOR BETA-ENDORPHIN.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

SUBLIARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                  1 YTKMKTATNIYIFNLALADALVTTTMPFQSTVYLMNSWPFGDVLCKIVISIDYYNMFTSI 60
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -B., JOHNSON P.S., PERSICO A.M., HAWKINS A.L., GRIFFIN C.A.,
                                                                                                                                                                                                                                                                      273 RNLRRITRMVLVVVAVFIVCWTPIHIYVIIKALITIPETTFQTVSWHFCIALGYTNSCLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Human mu opiate receptor. cDNA and genomic clones, pharmacologic characterization and chromosomal assignment.";
                                                                                                                                                                                                                                                                                                                 215 -IDCTLTFSHPTW-YWENLLKICVFIFAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                           . 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MESTEK A. UR., HURLEY J.H., BYE L.S., CAMPBELL A., TIAN M., CHEN Y., YU L.;
                                                                                                                      Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333 PVLYAFLDENFKRCFREFCIPTSSIIEQONSTRVRQNTREHPSTANTVD 381
                                         E -> G (IN REF. 6).
V -> I (IN REF. 3, 4 AND 7).
LENLE -> KIVLF (IN REF. 8).
; 2C21013D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBMITTED (XXX-1994) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1522; DB 1; L
Pred. No. 5.72e-282;
45; Mismatches 49;
               POTENTIAL. POTENTIAL.
   POTENTIAL.
38 PO
46 PO
53 PO
237 F
2437 V
391 LE
44494 MW;
                                                                                                                             Query Match
Best Local Similarity 66.1%;
Matches 191; Conservative
   38
46
237
245
245
387
398 AA;
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US-08-455-683-12.rsp

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OPRM1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 YTKMKTATNIYIFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNLRRIIRMYLVVVAVFIVCWTPIHIYVIIKALVTIPETTFQTVSWHFCIALGYTNSCLN 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 -IDCTLIFSHPIW-YWENLLKICVFIFAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VIECCLQFPDDDYSWWDLFWKICVF1FAFVIPVLIIIVCYTLMILRLXXXRLLSGSREKD
                                                                                                                               MINA, OCOLE, PSO0237; G_PROTEIN_RECEPIOR; 1.
PRAM; PF00001; 7tm_1; 1.
G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; PHOSPHORYLATION; LIPOPROTEIN; PALMITATE; ALTERNATIVE SPLICING. DOMAIN
1 66
EXTRACELULAR (POFENTIAL).
                                                                                                                                                                                                                                                                                                                                                                         -> VRS (IN MOR1A)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 400;
                                                                                                                                                                                                                                 4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

PAMMITATE (POTENTIAL).
                                                                                                                                                                               1 (POTENTIAL).
CTTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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D -> N (IN REF. 1).
M -> I (IN REF. 1).
L -> V (IN REF. 1).
7; 1AFC0337 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVLYAFLDENFKRCFREFCIPTSSNIEQQNSTRIRQNTRD 374
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1522; DB 1;
Pred. No. 5.72e-282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     43; Mismatches
                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
LENLEAETAPLP
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                                                                     EMBL, L25119, G452073, --
EMBL, L29301, G459832, --
EMBL, U12569, G607912, --
GCRDB, GCR_0885, --
GCRDB, GCR_2086, --
GCRDB, GCR_2042, --
                                                                                                                                                                                                                                                                                                                                                                                                                                   68.3%;
larity 67.1%;
Conservative
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48
400
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400 AA;
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Best Local Similarity
Matches 188; Conser
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97
105
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TRANSMEM
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 -IDCALTESHPTW-YWENLLKICVFIFAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKD 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILCIMSVDRYIAVCHPVKALDFRIPRNAKIINVCNWILSSAIGLPVMFMATIKYRNG-S 217
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

TISSUB-BRAIN CORIEX;

PAMPUSCH M.P., OSINSKI M.A., BROWN D.R., MURTAUGH M.P.,

SUBMITTED (NOV-1995) TO EMBL/GENBANK/DD3J DATA BANKS.

-I- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM

ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR

FOR BETA-ENDORPHIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROIEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM, PF00001; 7tm_1; 1.
G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; PHOSPHORYLATION; LIPOPROTEIN; PALMITAIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
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2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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Pred. No. 3.97e-281;
                                                      01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
MU-TYPE OPIOID RECEPTOR (MOR-1).
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6786FD94 CRC32;
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PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
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OPRM_PIG
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Matches
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 276 RNERRITRMVLVVVAVRIVCWTPIHIYVIIKALITIPBTTFQTVSWHFCIALGYTNSCLN 335
                                                 IISSUE-STRIATUM;
SIMON E.J., VILLEM S., ANDRIA M., ONOPRISHVILI I., HILLER J.M.;
SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BARKS.
-!- FONCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDCING CALCIUM
ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
FOR BETA-ENDORPHIN.
                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                            BOS TAURUS (BOVINE).
EUKRRYOTA, METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; BOSINAE; BOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 401;
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLEARMIC (POIENTIAL).
2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
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                                                                                      375
                                                                                                        241 PILYAFLDENFKRCFRDFCFPLKMXMERXSTSRVRNIVQD 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1489; DB 1;
Pred. No. 5.00e-275;
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5673B9B8 CRC32;
                                                                                      PVLYAFLDENFKRCFREFCIPTSSTIEQQNSARIRQNTRD
                                                                                                                                                                                    15-UUL-1998 (REL. 36, CREATED)
15-UUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-UUL-1998 (REL. 36, LAST REQUENCE UPDATE)
MU-TYPE OPIOID RECEPTOR (MOR-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 (POTENTIAL).
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E; PS00237; G_PROTEIN_RECEPTOR; 1.
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                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION;
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Best Local Similarity

Query Match

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                                                                                                                                                                                                                                335
                                                                                                                                                                                                                                                                181 XNLRRITRLVLVVVAVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYXFCIALGYTNSSLN 240
                                                                                                                LANNES B., MICHELETTI G., KIEFFER B.;
"The human delta-opioid receptor: genomic organization, cDNA cloning,
functional expression, and distribution in human brain.";
MOL. PHARMACOL. 46:1015-1021(1994).
                          99 YTKMKTATNIYIENFALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSI 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 FILCIMSVDRYIAVCHPVKALDLRIPRNAKIINICNWILSSAIGLPVMFMATIKYRQG-S
                                                                                                                                                                                    276 RNLRITRMYLVVVAVFIVCWTPIHIYVIIKALITIPETTFQTVSWHFCIALGYINSCLN
                                                                                                                                                                218 -IDSTLTFSHPTW-YWENLLKICVFIFAFIMPILIITVCYGLMILRLKSVRMLSGSKEKD
                                                          1 YTKMKTAINIYIFNLALADALVITIMPFQSTVYLMNSWPFGDVLCKIVISIDYYNMFTSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 95107267.
SIMONIN F., BEFORT K., GAVERLAUX-RUFF C., MATTHES H., NAPPEY V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNAPP R.J., MALAINSKA E., FANG L., LI X., BABIN E., NGUYEN M., SANTORO G., VARGA E.V., HRUBY V.J., ROESKE W.R., YAMAMURA H.I., "Identification of a human delta opioid receptor: cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                    336 PVLYAFLDENFKRCFREFCIPTSSTIEQQNSTRIRQNTRD 375
                                                                                                                                                                                                                                                                                                                                    241 PILYAFIDENFKRCFRDFCFPLKMXMERXSTSRVRNTVQD 280
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15-70L-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-70L-1998 (REL. 36, LAST ANNOTATION UPDATE)
DELTA-TYPE OPICID RECEPTOR (DOR-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; METAZOA; CHORDATA; VERTEBR;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
IISSUE-BRAIN CORIEX, AND STRIATUM;
MEDLINE; 94260835.
45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U07882; G497314; -.
EMBL; U10504; G501145; -.
EMBL; AL009181; E1250368; -.
GCRDB; GCR_1017; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIFE SCI. 54:463-469(1994).
 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPRD1 OR OPRD
                                                                                                                                                                                                                                                                                                                                                                                                            OPRD_HUMAN
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137
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                                                                                                                                                                                                                                                                                                             77 YIKMKTAINIYIFNLALADALAISTLPFQSAKYLMETWPFGELLCKAVLSIDYYNMFTSI 136
                                                                                                                                                                                                                                                                                                                                                FTLTMMSVDRYIAVCHPVKALDFRTPAKAKLINICIWVLASGVGVPIMVMAVTRPRDGA- 195
                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 93351652.
FUKUDA K., KATO S., MORI K., NISHI M., TAKESHINA H.;
"Primary structures and expression from cDNAs of rat opicid receptor
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                         VV-CMLQFPSPSW-YWDTVTKICVFLFAZVVPILIITVCYGLMLLRLRSVRLLSGSKEKD
                                                                                                                                                                                                                                                                                                                                                                                             RSLRRITRMVLVVVGAFVVCWAPIHIFVIVWTLVDIDRRDPLVVAALHLCIALGYANSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                RATIUS NORVEGICUS (RAI).
BUKARYOTA; METAZOA; CHORDAIA; VERTEBRAIA; MAMMALIA; BUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATIUS.
                                                                                                                                                                                                                                                                                Length 372;
                                                                                               3 (FOTBATIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
7 (POTENTIAL).
7 (POTENTIAL).
7 (POTENTIAL).
POTENTIAL).
POTENTIAL.
                    PRUSLIE: ECOUNTY TEMPERANE, BENODED RECEPTOR; TRANSMEMBRANE, GLYCOPROTEIN; G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; PALMITATE.

PROSPERRYLATION; LIPOPROTEIN; PALMITATE.

45 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                 Indels
                                                                                2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DELTA-TYPE OPIOID RECEPTOR (DOR-1) (OPIOID RECEPTOR A).
                                                               1 (POTENTIAL). CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                        BY SIMILARITY.

C -> F (IN REF. 1).

AR -> PG (IN REF. 1).

AR -> PG (IN REF. 1).

A -> P (IN REF. 1).
                                                                                                                                                                                                                                                                                                 33;
                                                                                                                                                                                                                                                                             Score 1458; DB 1;
Pred. No. 1.64e-268;
                                                                                                                                                                                                                                                                                               43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372 AA
GCRDB; GCR_2055; -.
MIM; 165195; -.
PROSITE: PS00237; G_PROIEIN_RECEPTOR; 1.
PFAM; PF00001; 7tm 1; 1.
                                                                                                                                                                                                POTENTIAL.
BY SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                            40368 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 NPVLYAFIDENFKRCFRQLC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 NPILYAFLDENFKRCFRDFC 259
                                                                                                                                                                                                                                                                             65.48;
                                                                                                                                                                                                                                                                                       69.28;
                                                                                                                                                                                                                                                                                   Local Similarity 69.2%;
les 180; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                            372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPRDI OR ROR-A.
                                                                      DOMAIN
TRANSMEM
                                                                                                       DOMAIN
TRANSMEM
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DOMAIN
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IRANSMEM
DOMAIN
                                                                                                                                                                                              CARBOHYD
DISULFID
                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ur 11
OPRD_RAT
P33533;
                                                                                                TRANSMEM
                                                                                                                                                   PRANSMEM
                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                        CONFLICT
                                                                                      DOMAIN
                                                                                                                         DOMAIN
                                                                                                                                                                                                               LIPID
                                                                                                                                                                                                                                                                                      Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                MEDLINE; 94322412.
ABOOD M.E., NOEL M.A., FARNSWORTH J.S., TAO Q.;
"Molecular cloning and expression of a delta-opioid receptor from rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 YTKLKTATNIYIFNLALADALATSTLPFQSAKYLMETWPFGELLCKAVLSIDYYNMFTSI 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILTMMSVDRYIAVCHPVKALDFRTPAKAKLINICIWVLASGVGVPIMVMAVTQPRDGA- 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 FILTHWASVDRYIAVCHPVRALDFRIPLKAKIINICIWLLSSSVGISAIVLGGTKVREDVD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- FUNCTION: INHIBITS NEURTRANSMITTER RELEASE BY REDUCING CALCIUM ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY STEREOSELECTIVE. RECEPTOR FOR ENKEPHALINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                    SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 VV-CILQFPSPSW-YMDTVTKICVFLFAFVVPILIITVCYGLMLLRLRSVRLLSGSKEXD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RSLRRITRMVLVVVGAFVVCWAPIHIFVIVWTLVDINRRDPLVVAALHLCIALGYANSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1452; DB 1; Length 372;
Pred. No. 2.99e-267;
44; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROBLES, SULLOSON, G_PROTEIN_RECEPTOR, 1.
PRAM: PF00001; 7tm_1; 1.
G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (POTENTIAL).

CYTOPLASKIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 (POTENTIAL).
EXTRACELUCIAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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59F5EE50 CRC32;
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                               SEQUENCE FROM N.A.
STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
                                                                                                                                                       J. NEUROSCI. RES. 37:714-719(1994)
delta- and mu-subtypes.";
FEBS LETT. 327:311-314(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.1%;
68.8%;
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D16348; G391865; -:
EMBL; U00475; G514211; -:
PIR; S34592; S34592.
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les 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3310
3310
3310
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCRDB; GCR_0638; -. GCRDB; GCR_0805; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33
121
333
372 AA;
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1003
1103
1105
1109
1109
111
18
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TRANSMEM
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TRANSMEM
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SEQUENCE
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DISULFID
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                                                                                                                                     brain.
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Matches
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LT 13
OPRX_RAT
P35370;
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TRANSMEM
DOMAIN
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TRANSMEM
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TRANSMEM
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B2DEGA I., CHIN H., KIM K., JUNG H.H., KOZAK C.A., KLEE W.A.; "Regional expression and chromosomal localization of the delta opiate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN ENG. 9:573-583(1996).

-!- FUNCTION: INHIBITS NETGOTRANSMITTER RELEASE BY REDUCING CALCIUM ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY STEREOSELECTIVE. RECEPTOR FOR ENKEPHALINS.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-!- TISSUE SPECIFICITY: BRAIN, WITH HIGH CONCENTRATIONS IN THE BASAL GANGILA AND LIMBET RECEIVE.

-!- SIMILARITY: BELONGS TO FAMILY I OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                           KIEFFER B.L., BEFORT K., GAVERIAUX-RUFF C., HIRTH C.G.;
"The delta-opioid receptor: isolation of a cDNA by expression cloning and pharmacological characterization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEITH D.E. JR., ANTON B., EVANS C.J.; "Characterization and mapping of a delta opioid receptor clone from
                                                                                                                                                                                                                                                                                                                              К.Н.;
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 93342064.
TASUDA K., RAYNOR K., KONG H., BREDER C.D., TAKEDA J., REISINE T.,
BELL G.I.;
                                                                                                                                                                                                                                                                                                     SECUENCE FROM N.A.
MEDLINE; 93110361.
EVANS C.J., KETHE D.E. JR., MORRISON H., MAGENDZO K., EDWARDS R.
"Cloning of a delta opioid receptor by functional expression.";
SCIENCE 258:1952-1955(1992).
                                                                                                                                                                                 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning and functional comparison of kappa and delta opioid receptors from mouse brain."; PROC. NATL. ACAD. SCI. U.S.A. 90:6736-6740(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 97001837.
ALKORTA I., LOEW G.H.;
"A 3D model of the delta opioid receptor and ligand-receptor complexes.",
                                                                                                                                                                                                                                                                              PROC. NATL. ACAD. SCI. U.S.A. 89:12048-12052(1992).
                                                                                                              01-001-1993 (REL. 27, CREATED)
01-001-1993 (REL. 27, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DELIA-TYPE OPICID RECEPTOR (DOR-1) (K56) (MSL-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROC. NAIL. ACAD. SCI. U.S.A. 90:9305-9309(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROC. WEST. PHARMACOL. SOC. 36:299-306(1993).
                                                                                       372 AA.
                                                                                        PRT;
                 314 NPVLYAFLDENFKRCFRQLC 333
                             240 NPILYAFLDENFKRCFRDFC 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 8-372 FROM N.A.
                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [6]
3D-STRUCTURE MODELLING.
                                                                                                                                                                          MUS MUSCULUS (MOUSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94022364.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                       OPRD_MOUSE
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 FILIMMSVDRYLAVCHPVKALDFRTPAKAKLINICIWVLASGVGVPIMVMAVTQPRDGA- 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VV-CMLQFPSPSW-YWDTVTKICVFLFAFVVPILIITVCYGLMLLRLRSVRLLSGSKEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 RSLRRITRMVLVVVGAFVVCWAPIHIFVIVWTLVDINRRDPLVVAALHLCIALGYANSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
NOCICEPTIN RECEPTOR (CRPHANIN FQ RECEPTOR) (KAPPA-TYPE 3 OPIOID
RECEPTIN (KOR-3) (ROR-C) (XOR1).
                                                                       EMBL; LOUZ21; 0192719.

R EMBL; LOUZ21; 0348247.

R EMBL; S6535; 6442326; -.

R EMBL; S6535; 6442326; -.

R EMBL; S6535; 6442326; -.

R EMBL; S6535; 64227; 848227.

R PIR; B48227; B48227.

R GCRDB; GCR_0429; -.

R GCRDB; GCR_0429; -.

R GCRDB; GCR_0429; -.

R GCRDB; GCR_0634; -.

R GCRDB; GCR_0634; -.

R GCRDB; GCR_0647; -.

R MGD; MGI:97438; OPRDI.

R PROSITE; PS0027; G_PROTEIN_RECEPTOR; 1.

R PROSITE; DS0027; G_PROTEIN_RECEPTOR; 1.

R PROM; PROOND; 7tm_1; 1.

R PROM; PROUND: 1.DPPROTEIN; DALMITATE.

N PROSHORYLATION; LIPPEROTEIN; DALMITATE.

N PROSHORYLATION; LIPPEROTEIN; DALMITATE.
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLUIAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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PALMITATE (POTENTIAL).
514022F5 CRC32;
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44; Mismatches 33;
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Pred. No. 2.07e-266;
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        entities requires a license agreement ( or send an email to license@isb-sib.ch)
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68.8%;
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EMBL, U05239, G451844; --
EMBL, U01313, G487965; --
EMBL, L028144; G49620; --
EMBL, U07871; G606803; --
EMBL, L29419, G57200; --
EMBL, L29419, G510719; --
PIR, S46238; S4638, PIR, S43655; GGRDB, GGR, 0834; --
GGRDB, GGR, 1030; --
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llarity 62.1%;
Conservative
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105
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367 AA;
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GCR_0898;
GCR_1030;
GCR_1030;
GCR_1455;
GCR_1455;
GCR_1517;
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receptor with
receptors.";
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                                                                                                                                                                                                                                    STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN; MEDLINE; 44307401.
BUNZOW J.R., SAEZ C., MORIRUD M., BOUVIER C., WILLIAMS J.T., LOW M., GRANDY D.K.; "Molecular cloning and tissue distribution of a putative member of the rat opioid receptor gene family that is not a mu, delta or kappa opioid receptor type."
                                                                                                                                                                                                                                                                                                                                                           CHEN Y., FAN Y., LIU J., MESTEK A., TIAN M., KOZAK C.A., YU L.; "Molecular cloning, tissue distribution and chromosomal localization of a novel member of the opioid receptor gene family."; FEBS LETT. 347:279-283(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                         SECURIOR: SEBRAIN;
MEDLINE; 95096849.
LACHOWICZ J.E., SHEN Y., MONSMA F.J. JR., SIBLEY D.R.;
"Molecular cloning of a novel G protein-coupled receptor related to the opiate receptor family.";
"Nemrochem. 64:34-40(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WICK M.J., MINNERATH S.R., LIN X:, ELDE R.P., LAW P.Y., LOH H.H.;
"Isolation of a novel cDNA encoding a putative membrane receptor wi
high homology to the cloned mu, delta, and kappa opioid receptors."
BRAIN RES. MOL. BRAIN RES. 27:37-44(1994).
-1- FUNCTION: RECEPTOR FOR THE NEUROPEPTIDE NOCIPEPTIN/ORPHANIN FO.
HAS A POTENTIAL ROLE IN MODULATING A NUMBER OF BRAIN FUNCTIONS,
INCLUDING INSTINCTIVE BEHAVIORS AND EMOTIONS. THE ACTIVITY OF
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TISSUE SPECIFICITY: HIGHLY EXPRESSED IN SEVERAL BRAIN AREAS.
SIMILARIIY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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S
                                                               SIRAINWISTAR; TISSUE=BRAIN; MEDLINE; 94215703.

MEDLINE; 94215703.

FURUDA K., KATO S., MORI K., NISHI M., TAKESHIMA H., IWABE N., MIYATA T., HOUTANI T., SUGIMOIO T.;

"CDNA cloning and regional distribution of a novel member of the opioid receptor family.";

FEBS LETT. 343:42-46(1994).
                                                                                                                                                                   TISSUE-HIPPOCAMPUS;
MENG F., XIE G., ALFRED M., THOMPSON R., HOVERSTEN M., WAISON
OPRLI OR OOR.
RAITOS NORVEGICUS (RAT).
BUKAKYOTA: METAZOA: CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RAITUS.
                                                                                                                                                                                                   SUBMITTED (JAN-1994) TO EMBL/GENBANK/DDBJ DATA BANKS
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FEBS LETT. 347:284-288(1994).
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSTIES, PROGRESS, G. PROTEIN_RECEPTOR; 1.
PRSP, 234996, 1DD.
G-PROTEIN COUPLED RECEPTOR; IRANSMENARE, GLYCOPROTEIN;
PHOSPHORYLATION, LIPOPROTEIN; PALMITATE.
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EXIRACELLULAR (POTENTIAL).
3 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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EXIRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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PALMITATE (POTENTIAL).
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REF. 3
CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 95318231.
HALFORD W.P., GEBHARDI B.M., CARR D.J.J.;
"Functional role and sequence analysis of a lymphocyte orphan opioid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: RECEPTOR FOR THE NEUROPEPTIDE NOCIPEPTIN/ORPHANIN FO. HAS A POTEWTIAL ROLLE IN MODDILATING A NUMBER OF ERAIN FUNCTIONS, INCLIDING INSTINCTIVE BEHAVIORS AND EMOTIONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENXLYL
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE; 9527076

MEDLINE; 9527076

BROOKS A.I., CHENG J., XU J., ROSSI G., JACOBSON E., RYAN-MORO J.,
BROOKS A.I., DEAN G.E., STANDIFER K.M., PASTERNAK G.W.;
"Cloning and functional characterization through antisense mapping
as kappa 3-related opioid receptor.";
MOL. PHARMACOL. 47:1180-1188(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 95100967.

NIGHI M., TAKESHIMA H., MORI M., NAKAGAWARA K.I., TAKEUCHI T.;

SILUCLURE and chromosomal mapping of genes for the mouse
kappa-opioid receptor and an opioid receptor homologue (MOR-C).";

BIOCHEM. BIOPHYS. RES. COMMUN. 205:1353-1357(1994).
                                                                                                              P35377; Q60645;
01-JUN-1994 (REL. 29, CREATED)
01-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
NOCICEPTIN RECEPTOR (ORPHANIN FO RECEPTOR) (KAPPA-TYPE 3 OPIOID RECEPTOR) (KOR-3) (ORGC) (K3 OPIATE RECEPTOR).
                                                                                                                                                                                                                                                MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAB; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MATTHES H.W.D., SEWARD E.P., KIEFFER B., NORTH R.A.; "Functional selectivity of orphanin FQ for its receptor coewith potassium channel subunits in Xenopus laevis occytes."
                                                                                                                                                                                                                                                                                                                                              STRAIN-CS7BL/6N; TISSUE-BRAIN;
YASUDA K., JONES E., REISINE I., BELL G.I.;
SUBMITTED (JAN-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
PAN Y.-X., XU J., PASTERNAK G.W.;
SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DAIA BANKS.
AA
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MEDLINE; 96387345.
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                                                                                                                                                                                   G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
                                                                                                                                                                                             PALMITATE.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                  1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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3F472156 CRC32;
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Pred. No. 2.23e-244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313 PILYAFLDENFKACFRKFCCASALHREMQVSDRVRSIAKD
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31, LAST SEQUENCE UPDATE)
37, LAST ANNOTATION UPDATE)
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                                                                                                              GCRDB; GCR_1/20,
GCRDB; GCR_1731; -.
GCRDB; GCR_1731; -.
MGD; MGI:97440; OPRL.
PROSITE; PS001237; G_PROTEIN_RECEPTOR; 1.
PPAM; PF00001; 7tm_1; 1.
PPAM; PF00001; 7tm_1; 1.
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                            , U22932, G1464791; -., U32928, G1464791; JOINED.

), U32930, G1464791; JOINED.

), U32930; G1464791; JOINED.

), U09421; G551468; -.
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        G808874; JOINED. G1008982; -.
                                                                                                                                                                                             PHOSPHORYLATION; LIPOPROTEIN;
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62.1%;
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Best Local Similarity 62.1%;
Matches 174; Conservative
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                                                                                                                                                                                                              LEE P.H., ZHU J., LIU-CHEN L., CHANG K.;
SUBMITTED (JAN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (JAN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-1- FUNCTION: RECEPTOR FOR THE NEUROPEPTIDE NOCIPEPTIN/ORPHANIN FQ.
HAS A POTENTIAL ROLE IN MODULATING A NUMBER OF BRAIN FUNCTIONS, INCLUDING INSTINCTIVE BEHAVIORS AND EMOTIONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENTLYI
                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                   MEDLINE; 94185768.
MOLLEREAU C., PARMENTIER M., MAILLEUX P., BUTOUR J.L., MOISAND C., FALALON P., CAPUT D., VASSART G., MEDNIER C.;
"ORLL, a novel member of the opioid receptor family. Cloning, functional expression and localization.";
FEBS LETT. 341:33-38(1994).
 NOCICEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR) (KAPPA-TYPE 3 OPIOID
                                                    CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLXCOPROTEIN; PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.

DOMAIN

1 50 EXTRACELLULAR (POTENTIAL).
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BE3C3E8F CRC32;
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PFAM; PF00001; 7tm_1; 1.
HSSP; P34996; 1DDD.
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                                                                  PRIMAIES; CATARRHINI; HOMINIDAE; HOMO
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PPR; S43087; S43087.
GCNDB; GCR_0987; --.
GCRDB; GCR_1988; --.
MIM; 602548; --.
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OPRLI OR ORLI OR OOR.
HOMO SAPIENS (HUMAN);
EUKARYOTA; METAZOA; CI
                                                                                                           TISSUE-BRAIN STEM;
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TLTAMSVDRYVAICHPIRALDVRTSSKAQAVNVAIWALASVVGVPVAIMGSAQV-EDEE-
                                                         62 TLTMMSVDRYIAVCHPVRALDFRTPLRAKIINICIWLLSSSVGISAIVLGGTKVREDVDV
                                                                                      IECLVEIPTPQDY-WGPVFA-ICIFLFSFIVPVLVISVCYSIMIRRLRGVRLLSGSREKD
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Conservative

Best Local Similarity
Matches 171; Conserv

Query Match

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